APPROVED O.G. FIG.
BY
CLASS SUBCLASS
DRAFTSMAN

Fig. 1

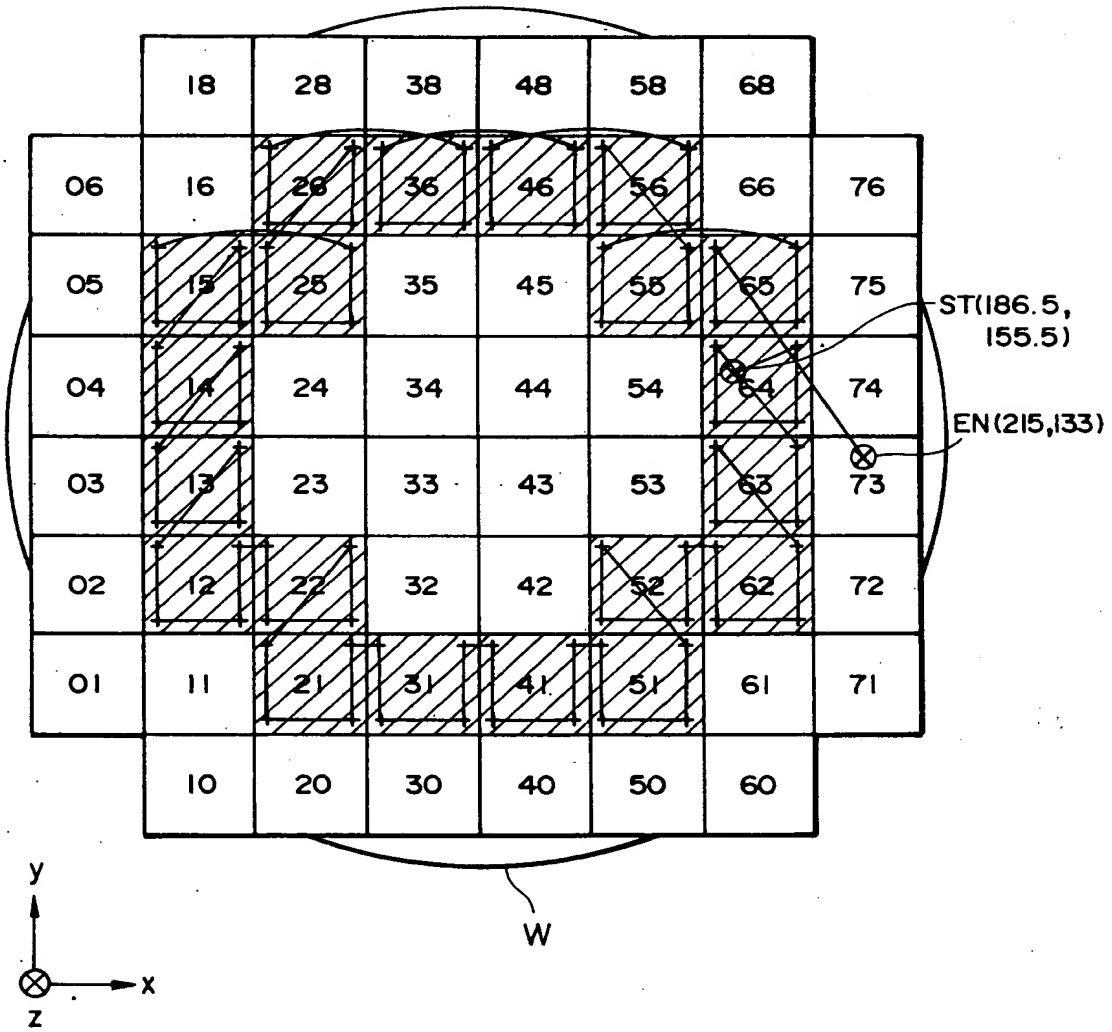
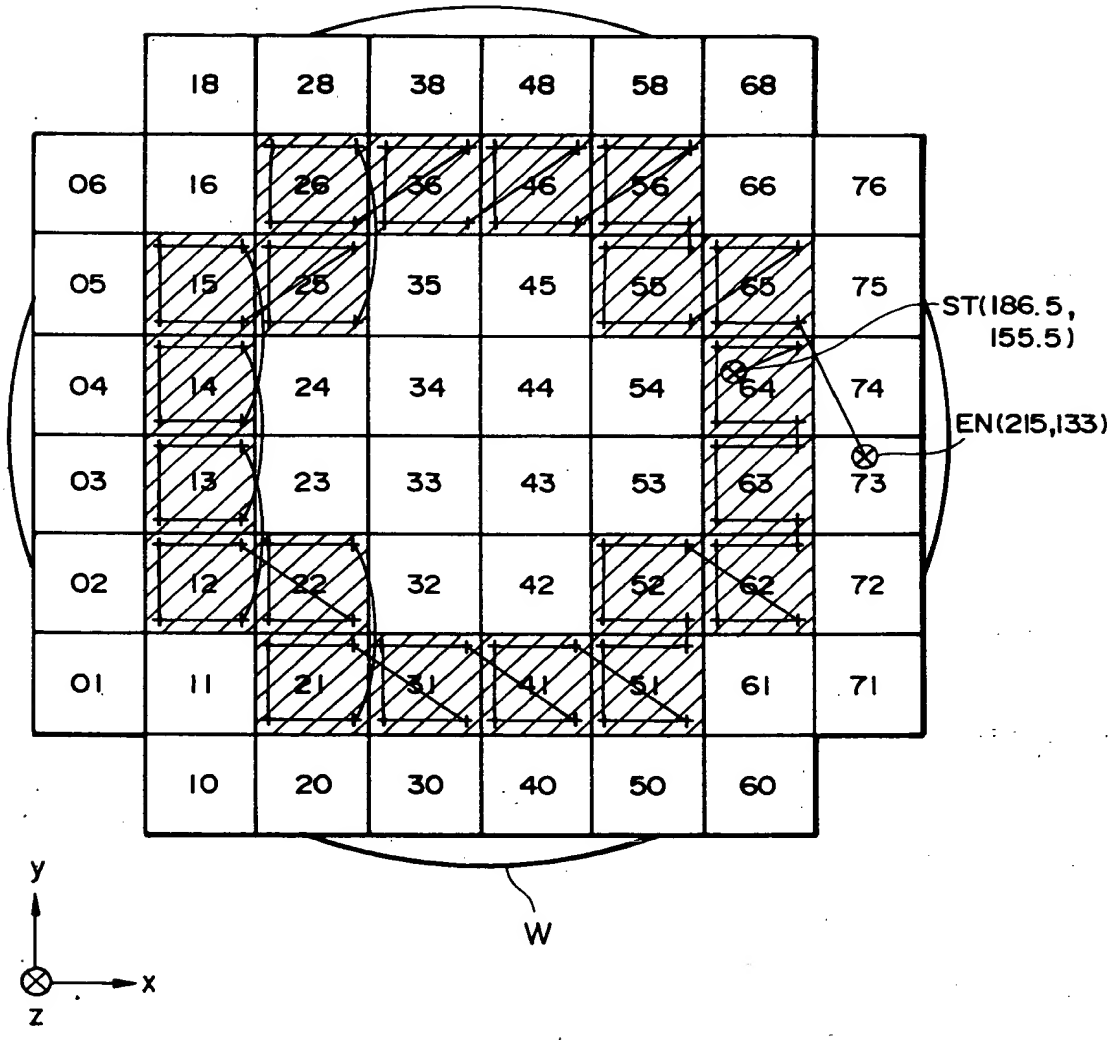


Fig. 2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ST(186.5, 155.5)
EN(215,133)
W
y
x
z

Title: METHOD OF DETERMINING MOVEMENT SEQUENCE, ALIGNMENT APPARATUS, METHOD AND APPARATUS OF DESIGNING OPTICAL SYSTEM, AND MEDIUM IN WHICH PROGRAM REALIZING THE DESIGNING METHOD
Inventor(s): Koji YOSHIDA, et al
DOCKET NO.: 061807-0137

Fig.3

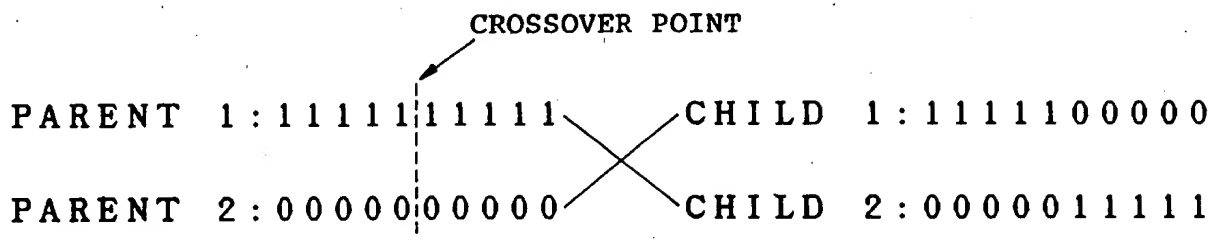


Fig.4

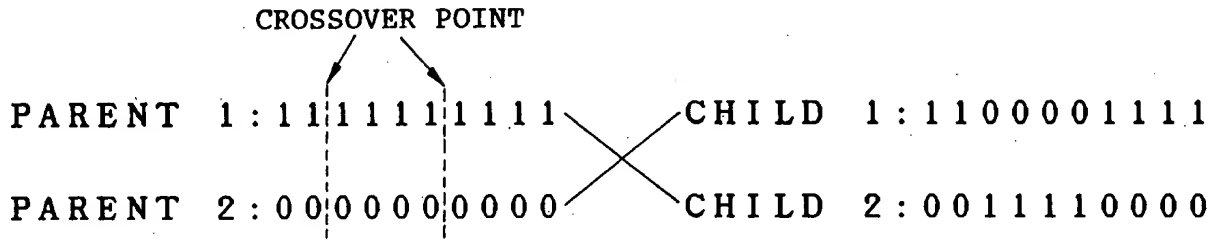


Fig.5

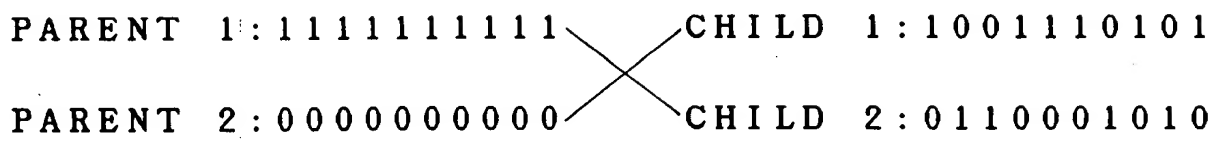
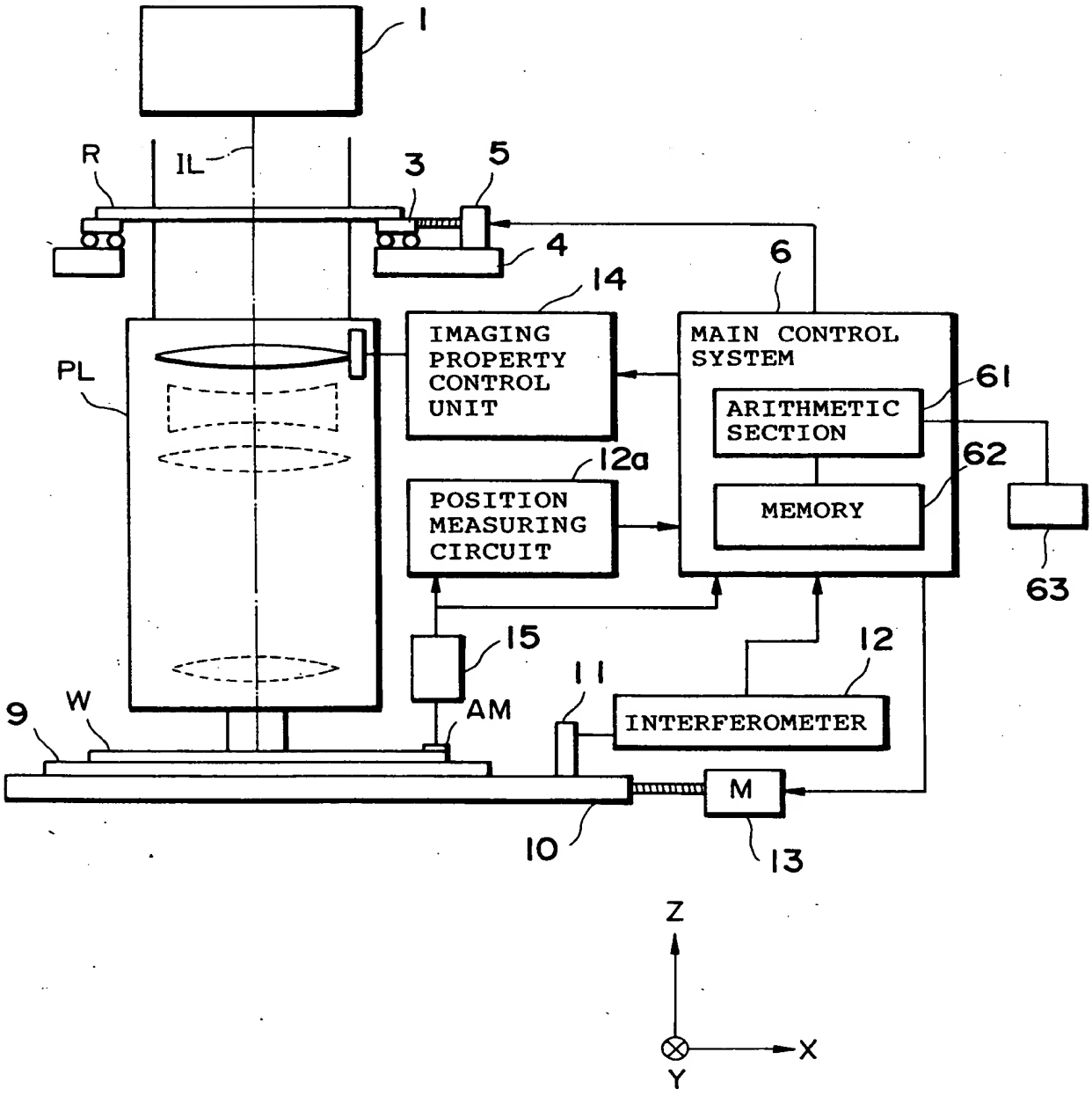


Fig.6


1
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IL
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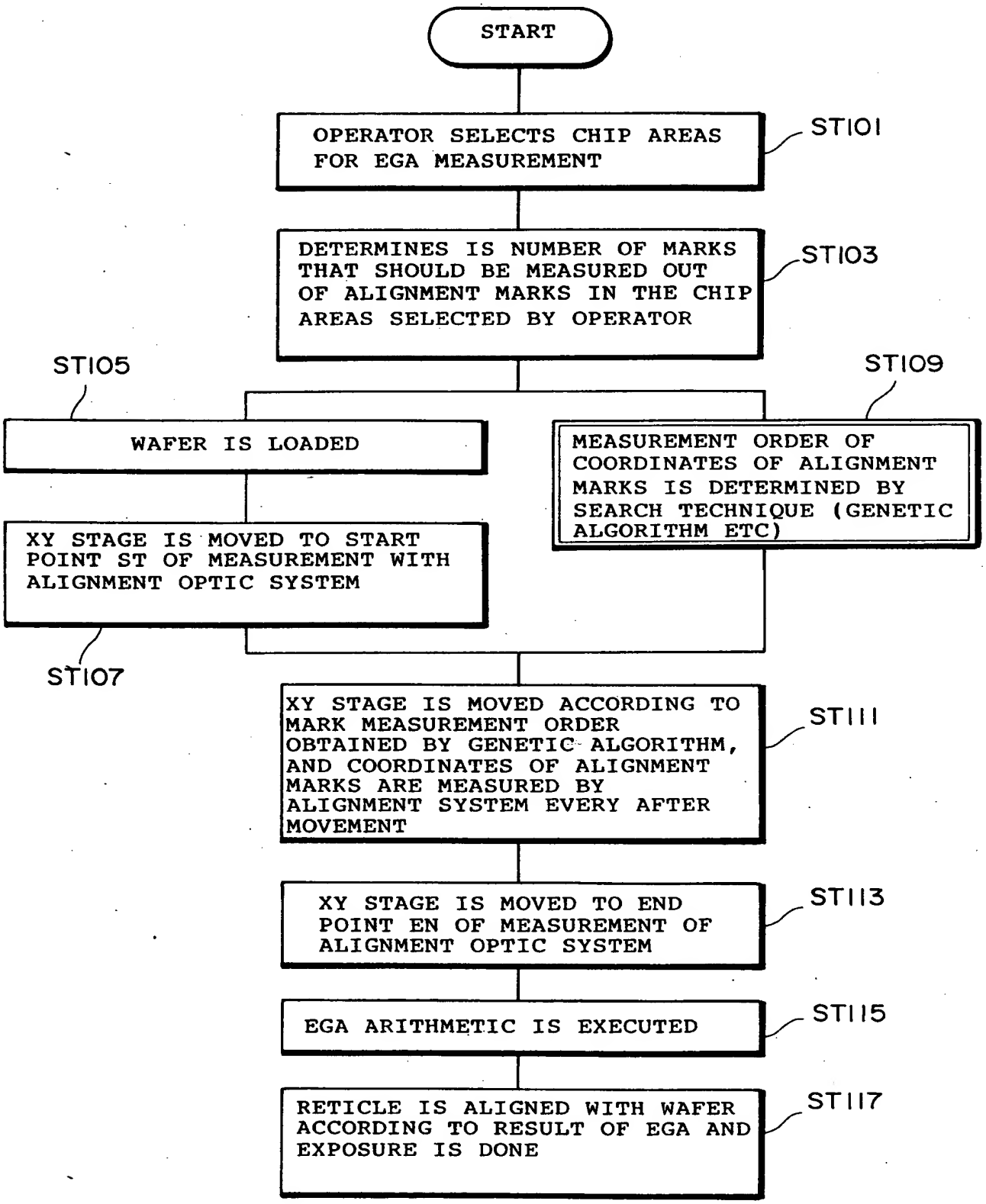
14
IMAGING PROPERTY CONTROL UNIT
MAIN CONTROL SYSTEM
61
ARITHMETIC SECTION
62
MEMORY
63
PL
12a
POSITION MEASURING CIRCUIT
15
12
11
9
W
AM
INTERFEROMETER
M
10
13
Z
X
Y

Fig. 7


START
OPERATOR SELECTS CHIP AREAS FOR EGA MEASUREMENT
ST101
DETERMINES IS NUMBER OF MARKS THAT SHOULD BE MEASURED OUT OF ALIGNMENT MARKS IN THE CHIP AREAS SELECTED BY OPERATOR
ST103
ST105
WAFER IS LOADED
XY STAGE IS MOVED TO START POINT ST OF MEASUREMENT WITH ALIGNMENT OPTIC SYSTEM
ST107
ST109
MEASUREMENT ORDER OF COORDINATES OF ALIGNMENT MARKS IS DETERMINED BY SEARCH TECHNIQUE (GENETIC ALGORITHM ETC)
XY STAGE IS MOVED ACCORDING TO MARK MEASUREMENT ORDER OBTAINED BY GENETIC ALGORITHM, AND COORDINATES OF ALIGNMENT MARKS ARE MEASURED BY ALIGNMENT SYSTEM EVERY AFTER MOVEMENT
ST111
XY STAGE IS MOVED TO END POINT EN OF MEASUREMENT OF ALIGNMENT OPTIC SYSTEM
ST113
EGA ARITHMETIC IS EXECUTED
ST115
RETICLE IS ALIGNED WITH WAFER ACCORDING TO RESULT OF EGA AND EXPOSURE IS DONE
ST117

Tue, 22 Jan 2002 15:00:00

Fig.8

ATTRIBUTE		VALUE OF PARAMETER SET IN EMBODIMENT
START POINT ST	X Y	186.5 (mm) 155.5 (mm)
END POINT EN	X Y	215 (mm) 133 (mm)
ACCELERATION OF WAFER STAGE 10	X Y	0.34g 0.2g
MAX SPEED OF WAFER STAGE 10	X Y	270 (mm/sec) 200 (mm/sec)
SETTLING TIME OF WAFER STAGE		0.032 (sec)
TIME NECESSARY FOR MEASURING COORDINATES OF ONE ALIGNMENT MARK		0.5 (sec)

g:ACCELERATION OF GRAVITY (=9.80m/sec)

Fig.9

CHIP AREA	COORDINATES OF CENTER	CHIP AREA	COORDINATES OF CENTER
12	(83、105)	41	(149、83)
13	(83、127)	46	(149、193)
14	(83、149)	51	(171、83)
15	(83、171)	52	(171、105)
21	(105、83)	55	(171、171)
22	(105、105)	56	(171、193)
25	(105、171)	62	(193、105)
26	(105、193)	63	(193、127)
31	(127、83)	64	(193、149)
36	(127、193)	65	(193、171)

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DOCKET NO.: 061807-0137

	START	12(1)	12(2)	12(3)	12(4)	13(1)	13(2)	
12(1)	0.378296	×	0.109449	0.132981	0.132981	0.142	0.142	
12(2)	0.45237	0.109449	×	0.132981	0.132981	0.142	0.142	
12(3)	0.45237	0.132981	0.132981	×	0.109449	0.242	0.242	
12(4)	0.378296	0.132981	0.132981	0.109449	×	0.242	0.242	
13(1)	0.378296	0.142	0.142	0.242	0.242	×	0.109449	
13(2)	0.45237	0.142	0.142	0.242	0.242	0.109449	×	
⋮				⋮				
64(3)	0.123721	0.36533	0.439407	0.439407	0.365333	0.365333	0.439407	
64(4)	0.123721	0.439407	0.513481	0.513481	0.439407	0.439407	0.513481	
65(1)	0.1595	0.439407	0.513481	0.513481	0.462	0.439407	0.513481	
65(2)	0.1595	0.36533	0.439407	0.462	0.462	0.365333	0.439407	
65(3)	0.084955	0.36533	0.439407	0.439407	0.365333	0.365333	0.439407	
65(4)	0.102346	0.439407	0.513481	0.513481	0.439407	0.439407	0.513481	
END	×	0.483852	0.557926	0.557926	0.483852	0.483852	0.557926	

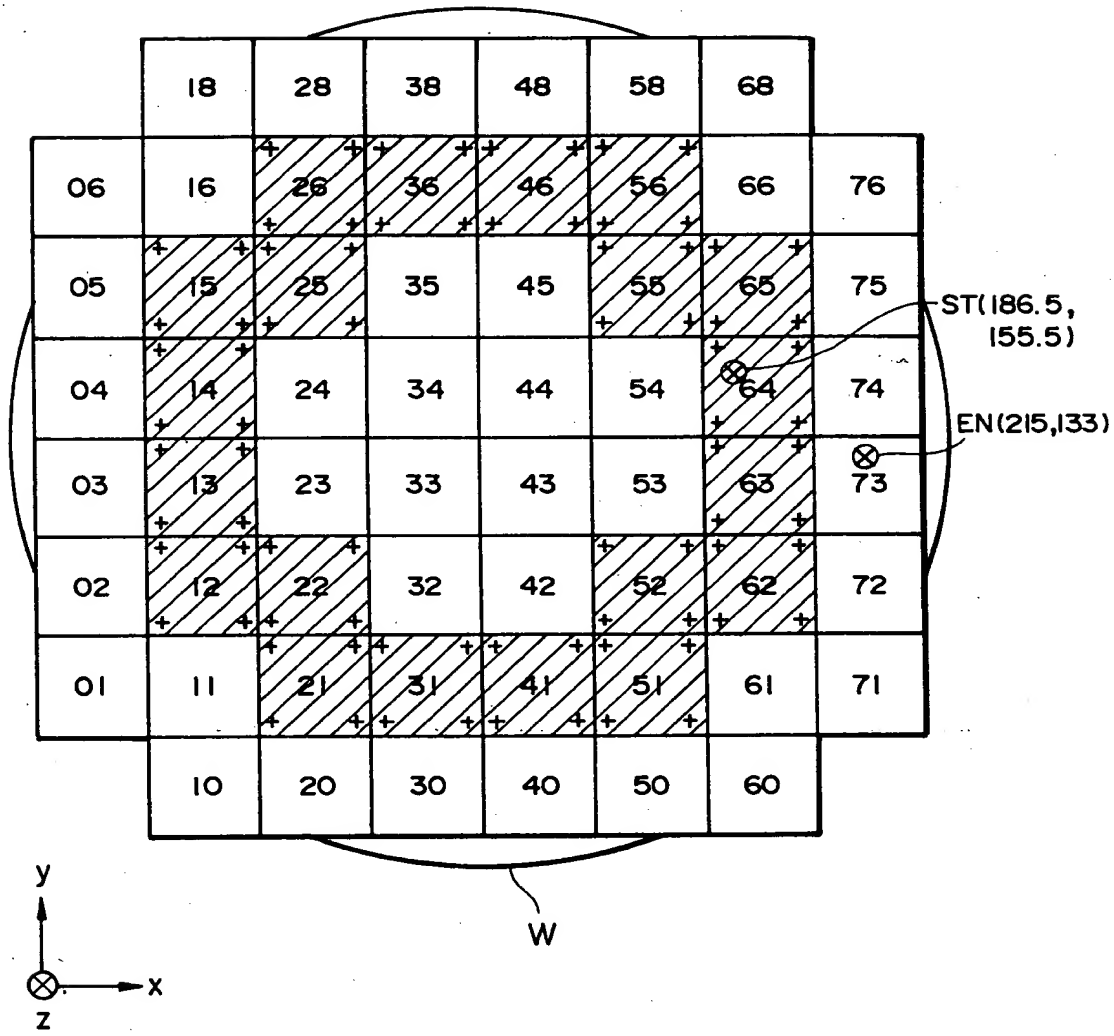
F

(UNIT:SEC)

	64(3)	64(4)	65(1)	65(2)	65(3)	65(4)
	0.365333	0.439407	0.439307	0.365333	0.365333	0.439407
	0.439407	0.513481	0.513481	0.439407	0.439407	0.513481
	0.439407	0.513481	0.513481	0.462	0.439407	0.513481
	0.365333	0.439407	0.462	0.462	0.365333	0.439407
	0.365333	0.439407	0.439407	0.365333	0.365333	0.439407
	0.439407	0.513481	0.513481	0.439407	0.439407	0.513481
			⋮			
	×	0.109449	0.242	0.242	0.142	0.142
	0.109449	×	0.242	0.242	0.142	0.142
	0.242	0.242	×	0.109449	0.132981	0.132981
	0.242	0.242	0.109449	×	0.132981	0.132981
	0.142	0.142	0.132981	0.132981	×	0.109449
	0.142	0.142	0.132981	0.132981	0.109449	×
	0.150519	0.091992	0.272	0.272	0.172	0.172

Fig. 10

Fig. 11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ST(186.5, 155.5)
EN(215,133)
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x
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Fig. 12

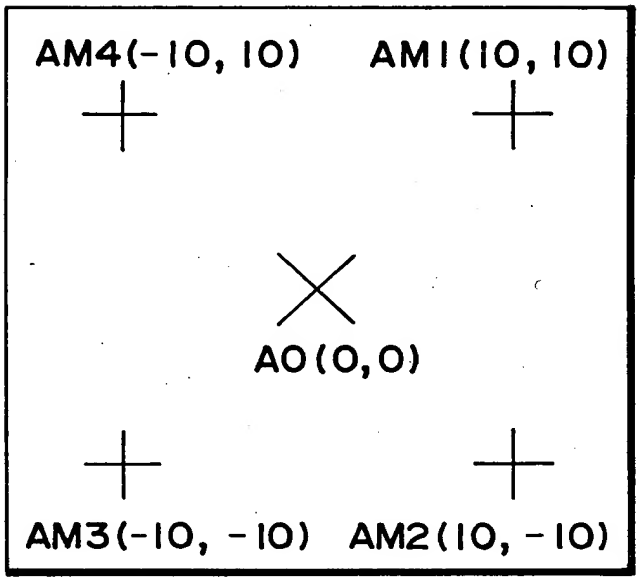

AM4(-10, 10)
AM1(10, 10)
AO(0,0)
AM3(-10, -10)
AM2(10, -10)

Fig. 13

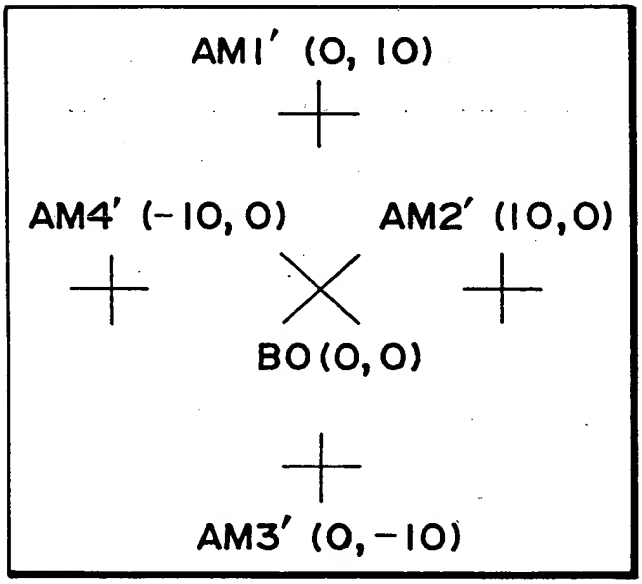

AM1' (0, 10)
AM4' (-10, 0)
AM2' (10,0)
BO(0,0)
AM3' (0,-10)

Fig. 14

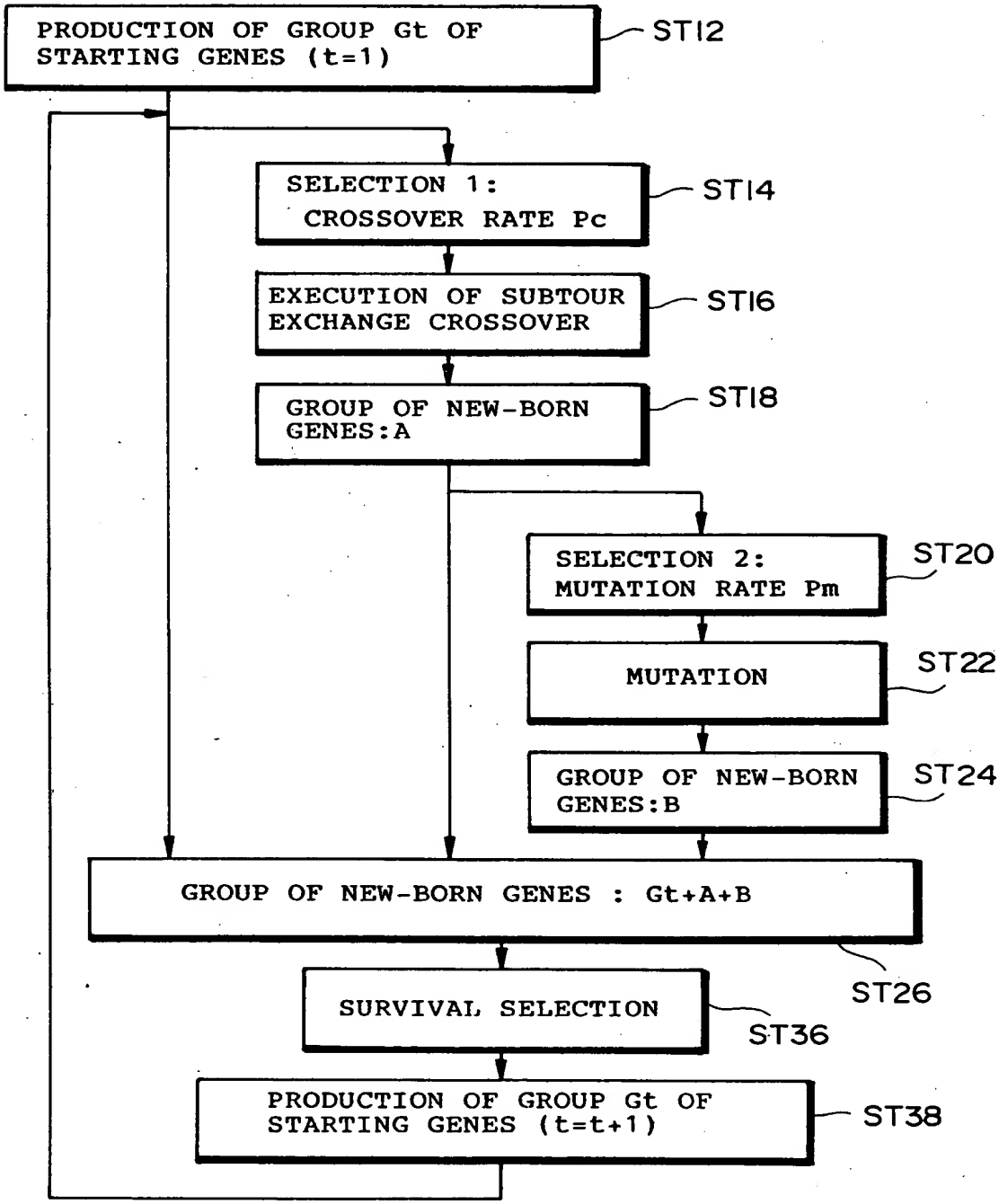

PRODUCTION OF GROUP Gt OF STARTING GENES (t=1)
ST12
SELECTION 1: CROSSOVER RATE Pc
ST14
EXECUTION OF SUBTOUR EXCHANGE CROSSOVER
ST16
GROUP OF NEW-BORN GENES:A
ST18
SELECTION 2: MUTATION RATE Pm
ST20
MUTATION
ST22
GROUP OF NEW-BORN GENES:B
ST24
GROUP OF NEW-BORN GENES : Gt+A+B
ST26
SURVIVAL SELECTION
ST36
PRODUCTION OF GROUP Gt OF STARTING GENES (t=t+1)
ST38

Fig. 15

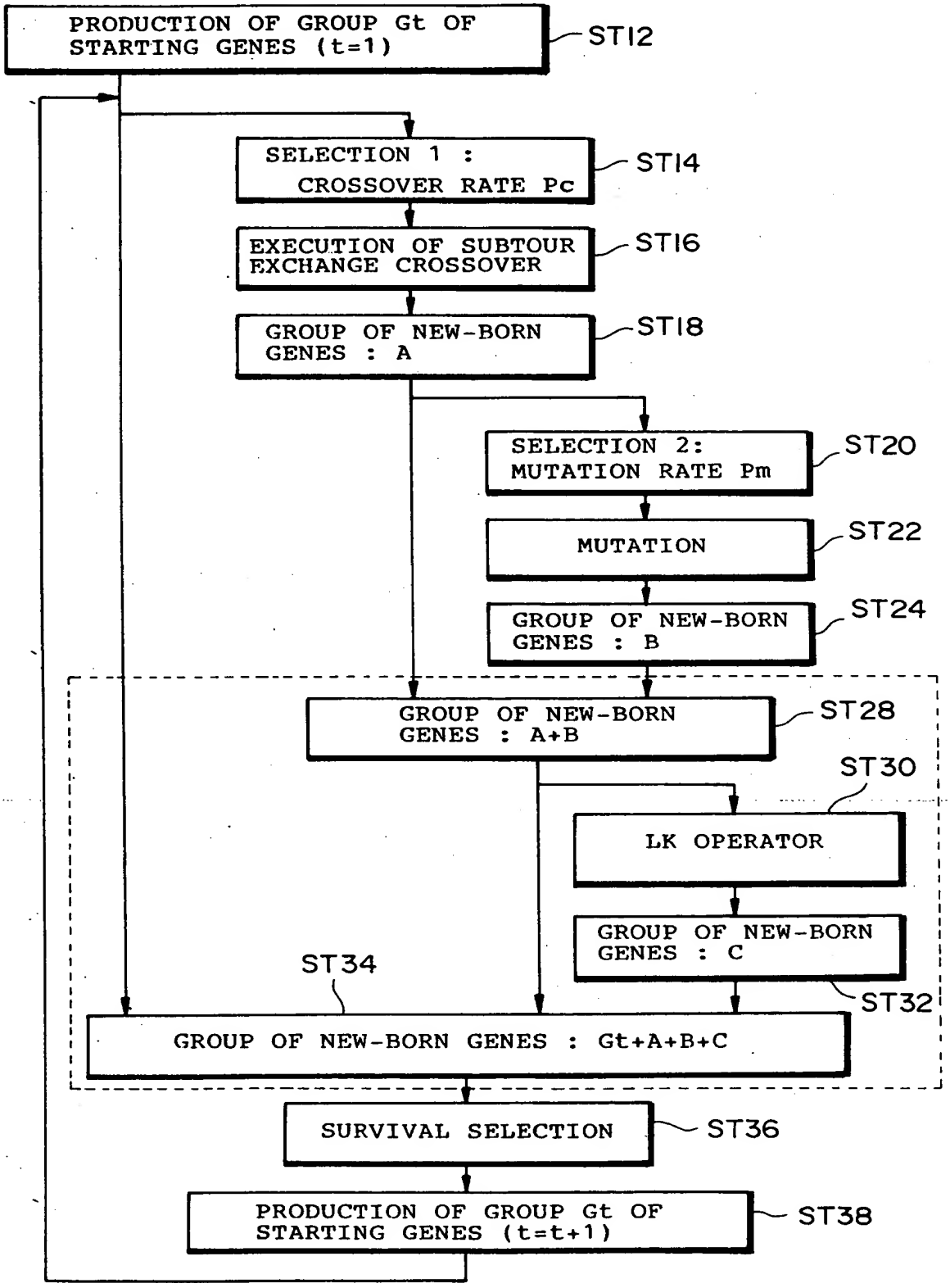

PRODUCTION OF GROUP Gt OF STARTING GENES (t=1)
ST12
SELECTION 1 : CROSSOVER RATE Pc
ST14
EXECUTION OF SUBTOUR EXCHANGE CROSSOVER
ST16
GROUP OF NEW-BORN GENES : A
ST18
SELECTION 2: MUTATION RATE Pm
ST20
MUTATION
ST22
GROUP OF NEW-BORN GENES : B
ST24
GROUP OF NEW-BORN GENES : A+B
ST28
ST30
LK OPERATOR
GROUP OF NEW-BORN GENES : C
ST32
ST34
GROUP OF NEW-BORN GENES : Gt+A+B+C
SURVIVAL SELECTION
ST36
PRODUCTION OF GROUP Gt OF STARTING GENES (t=t+1)
ST38

Fig. 16

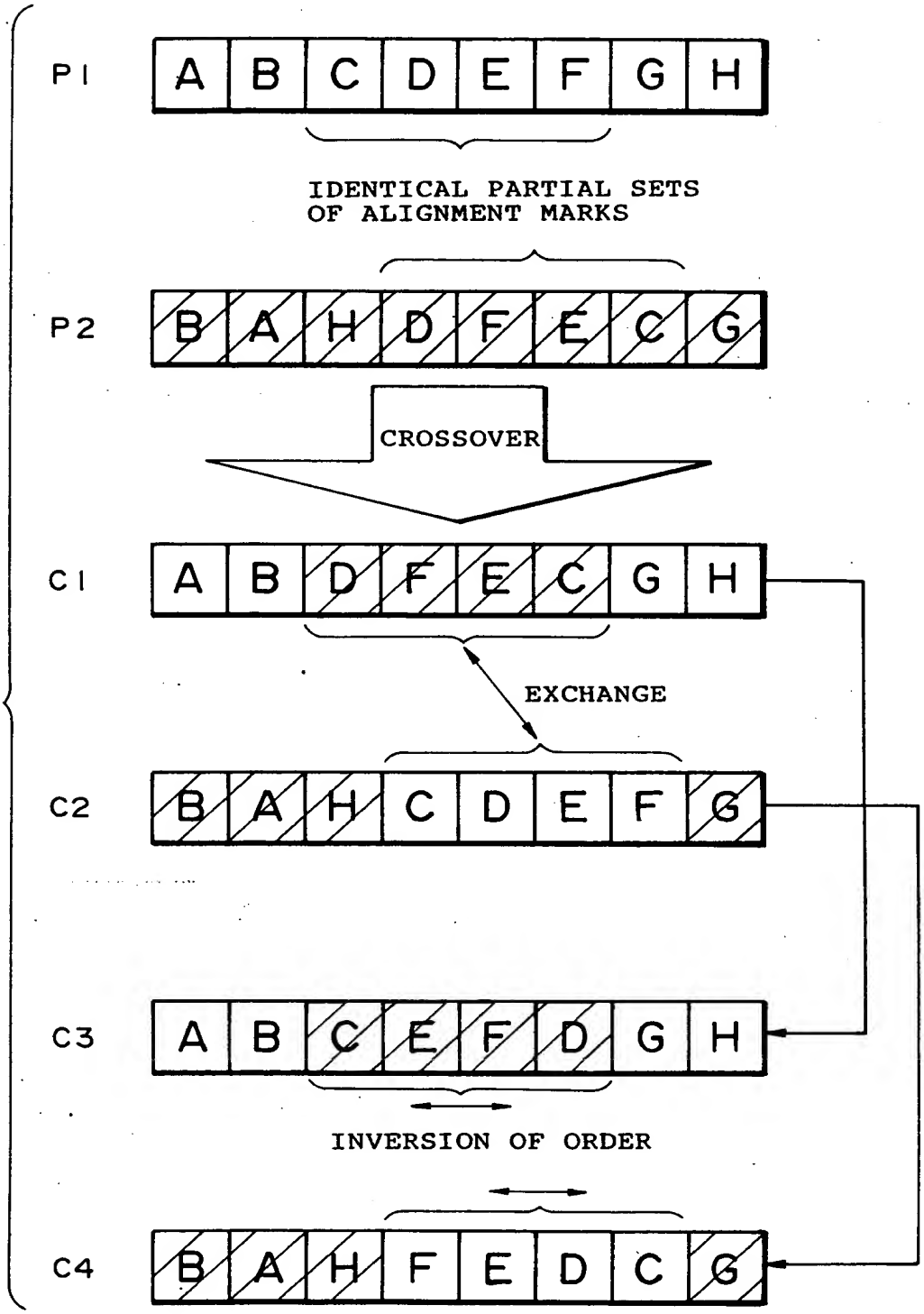

P1
A B C D E F G H
IDENTICAL PARTIAL SETS OF ALIGNMENT MARKS
P2
B A H D F E C G
CROSSOVER
C1
A B D F E C G H
EXCHANGE
C2
B A H C D E F G
C3
A B C E F D G H
INVERSION OF ORDER
C4
B A H F E D C G

Fig. 17

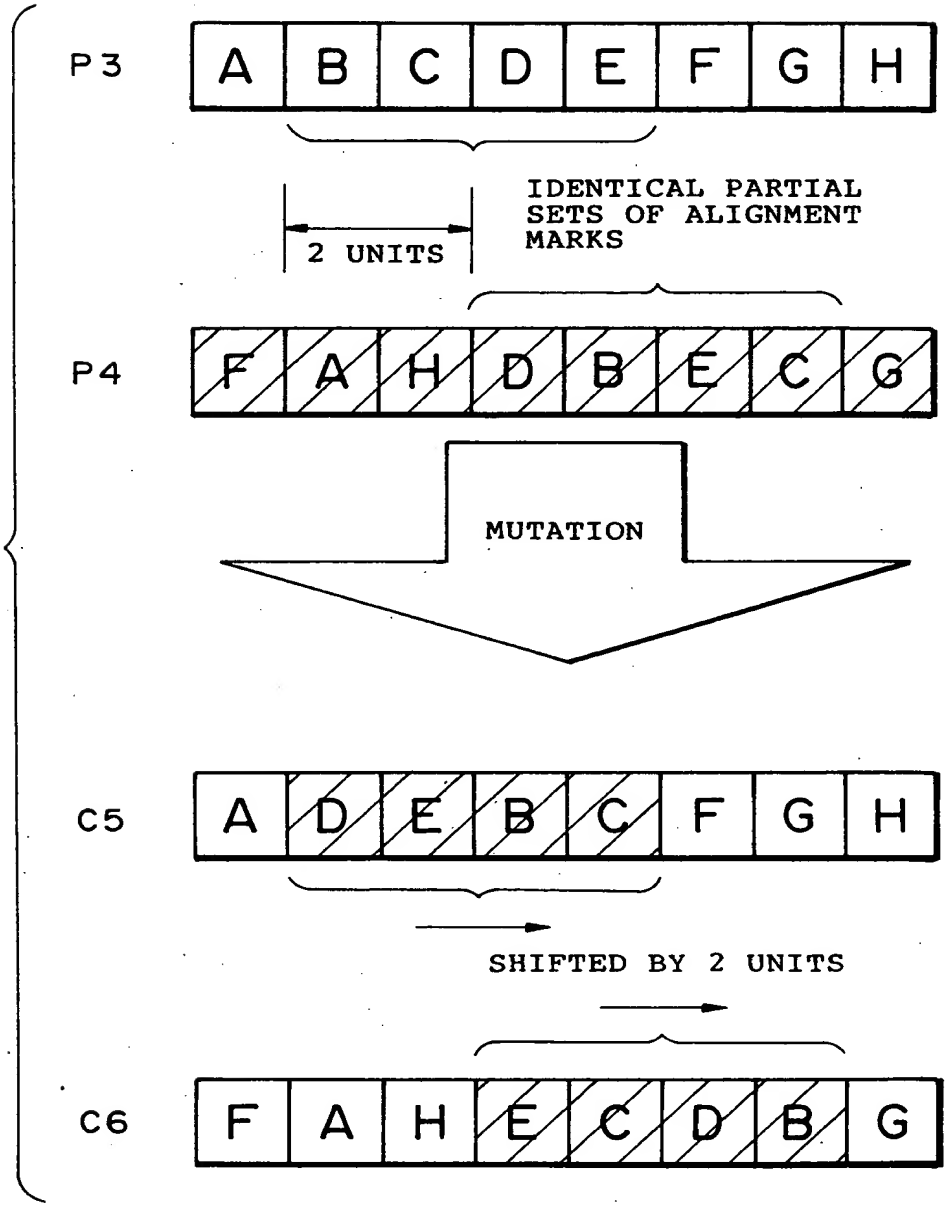
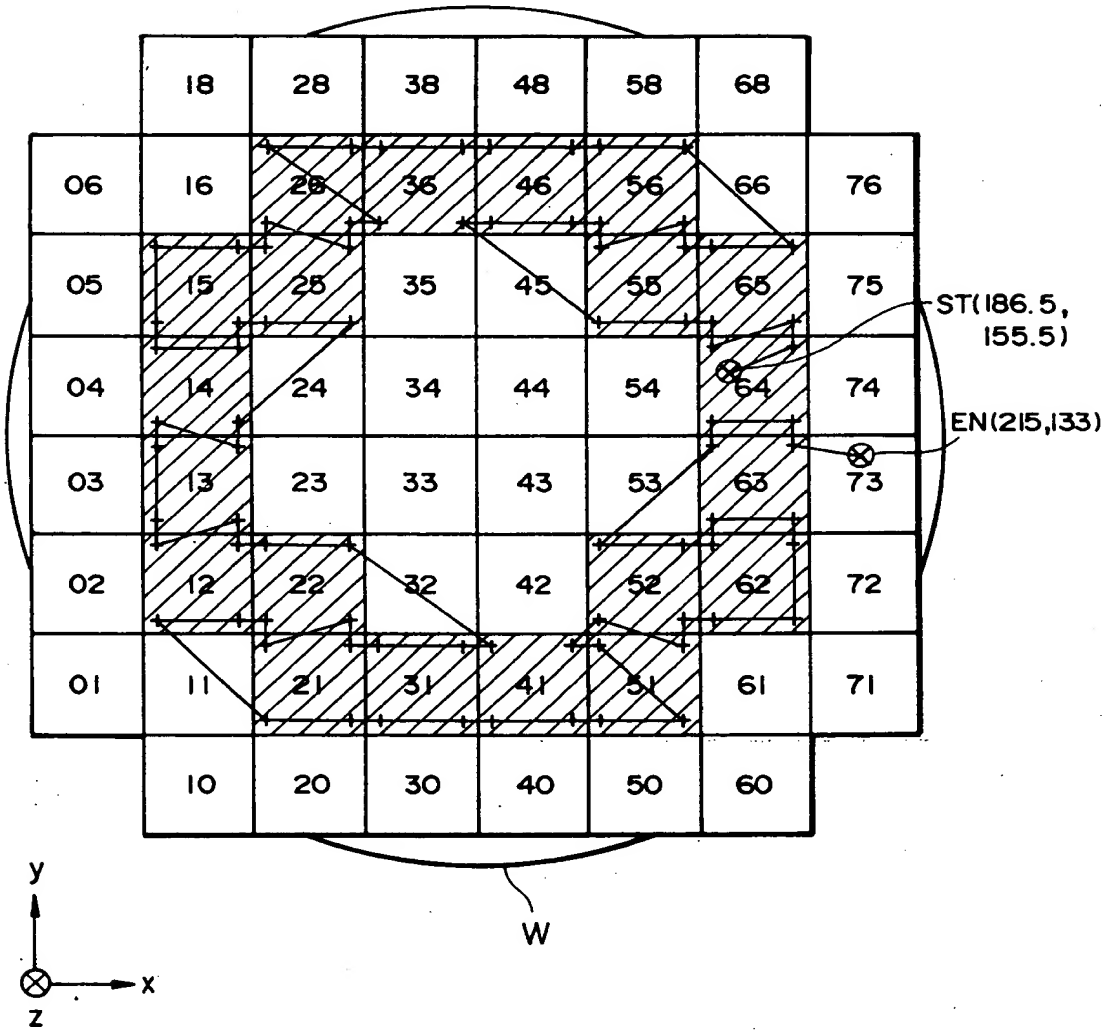

P3
A B C D E F G H
2 UNITS
IDENTICAL PARTIAL SETS OF ALIGNMENT MARKS
P4
F A H D B E C G
MUTATION
C5
A D E B C F G H
SHIFTED BY 2 UNITS
C6
F A H E C D B G

Fig. 18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ST(186.5, 155.5)
EN(215,133)
W
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x
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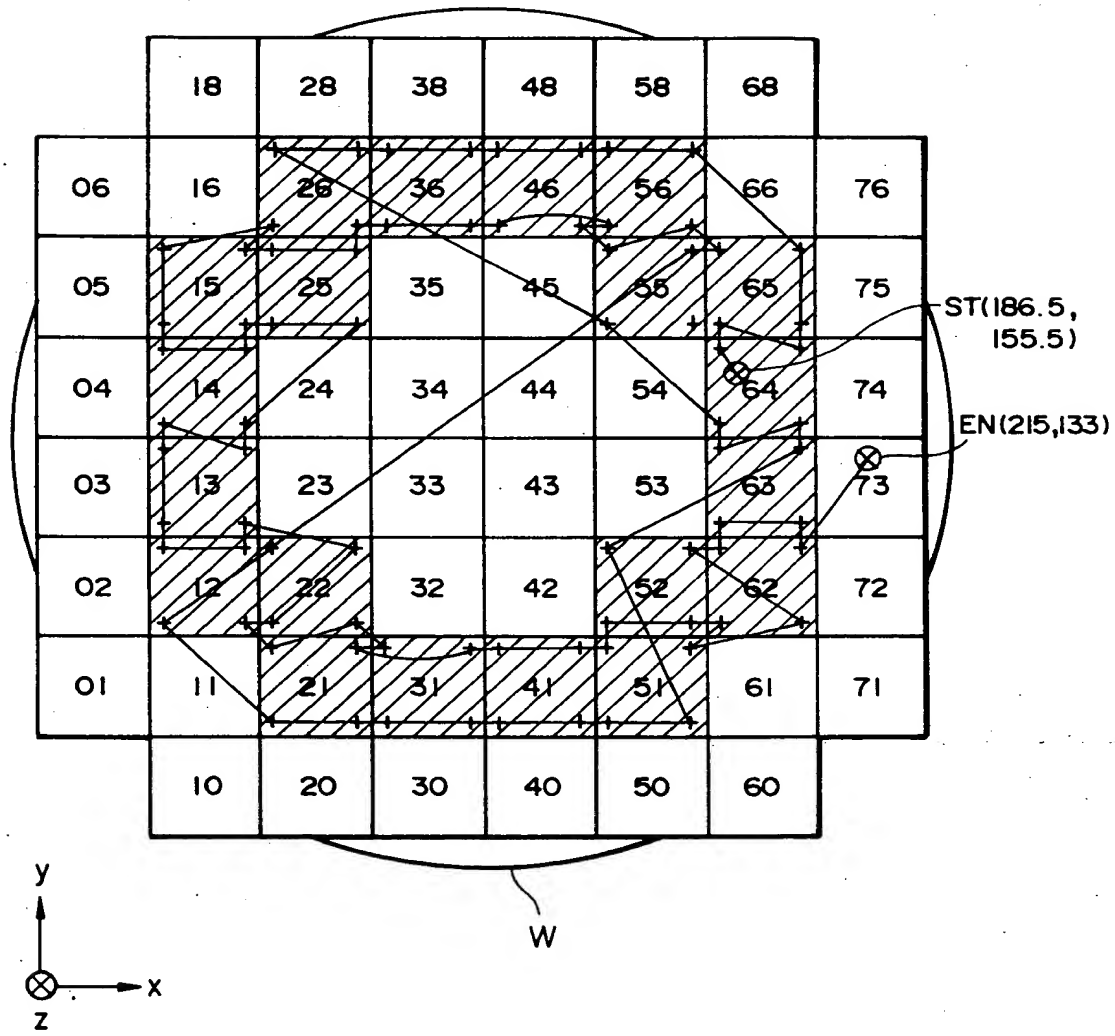
Fig. 19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72
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ST(186.5, 155.5)
EN(215,133)
W
y
x
z

Fig.20

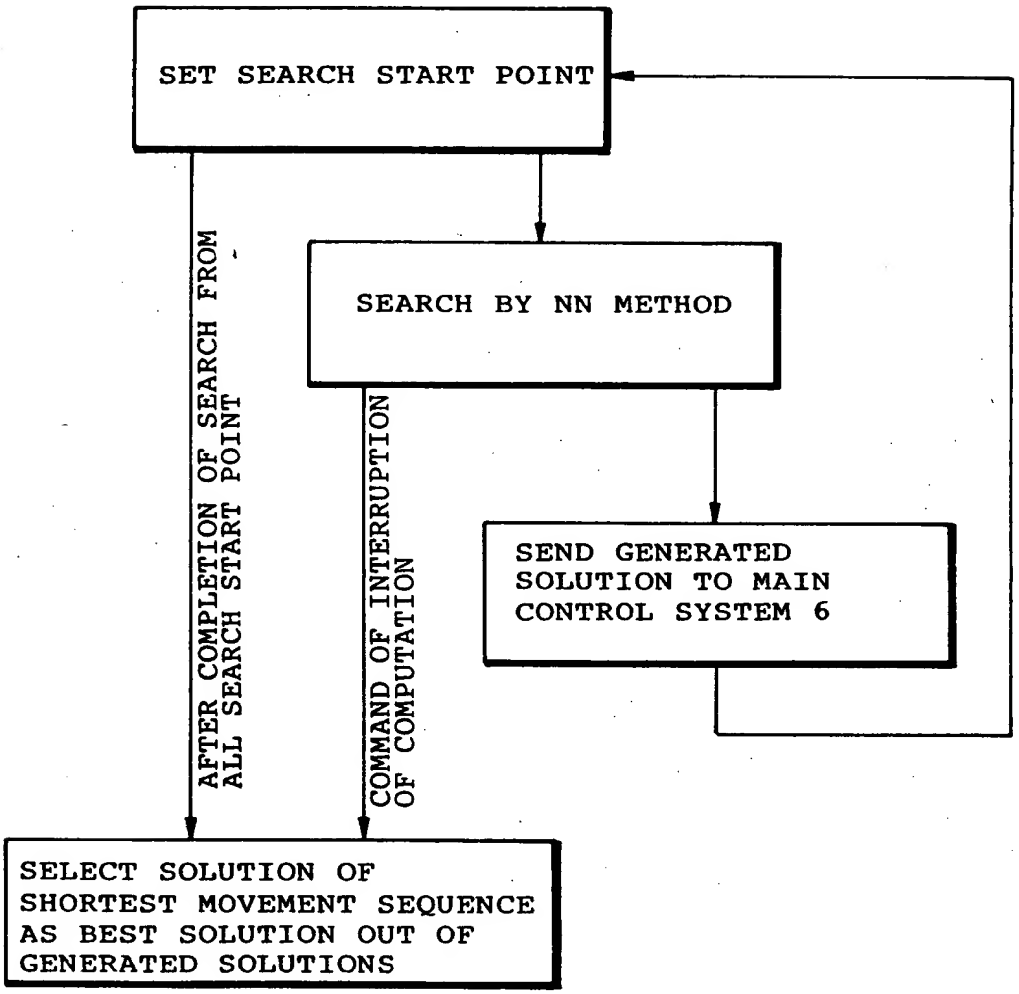
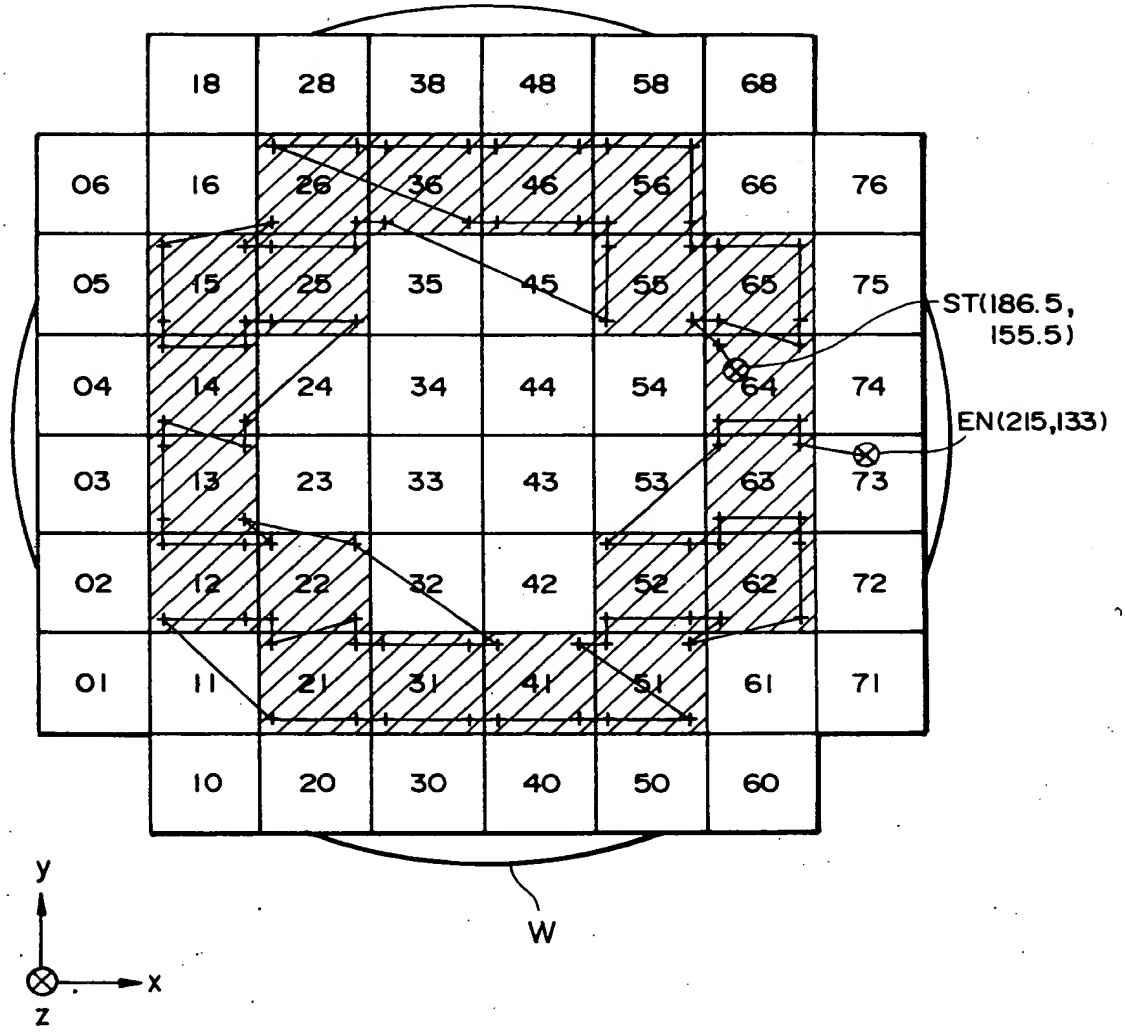

SET SEARCH START POINT
SEARCH BY NN METHOD
SEND GENERATED SOLUTION TO MAIN CONTROL SYSTEM 6
AFTER COMPLETION OF SEARCH FROM ALL SEARCH START POINT
COMMAND OF INTERRUPTION OF COMPUTATION
SELECT SOLUTION OF SHORTEST MOVEMENT SEQUENCE AS BEST SOLUTION OUT OF GENERATED SOLUTIONS

Fig.21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41
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ST(186.5, 155.5)
EN(215,133)
W
y
x
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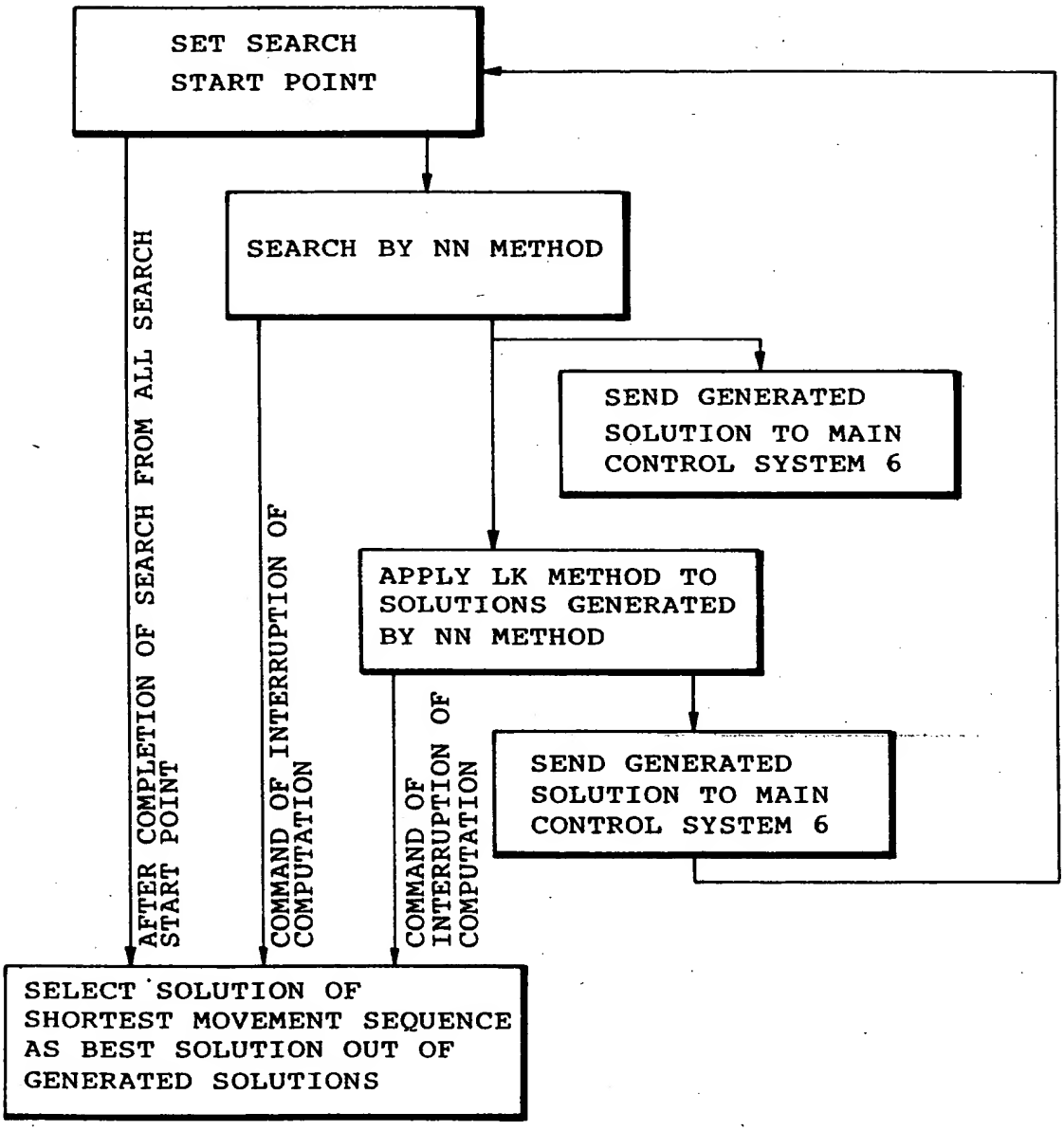
Fig.22


SET SEARCH START POINT
SEARCH BY NN METHOD
SEND GENERATED SOLUTION TO MAIN CONTROL SYSTEM 6
APPLY LK METHOD TO SOLUTIONS GENERATED BY NN METHOD
SEND GENERATED SOLUTION TO MAIN CONTROL SYSTEM 6
AFTER COMPLETION OF SEARCH FROM ALL SEARCH START POINT
COMMAND OF INTERRUPTION OF COMPUTATION
COMMAND OF INTERRUPTION OF COMPUTATION
SELECT SOLUTION OF SHORTEST MOVEMENT SEQUENCE AS BEST SOLUTION OUT OF GENERATED SOLUTIONS

Title: METHOD OF DETERMINING MOVEMENT SEQUENCE, ALIGNMENT APPARATUS, METHOD AND APPARATUS OF DESIGNING OPTICAL SYSTEM, AND MEDIUM IN WHICH PROGRAM REALIZING THE DESIGNING METHOD
Inventor(s): Koji YOSHIDA, et al
DOCKET NO.: 061807-0137

Fig.23

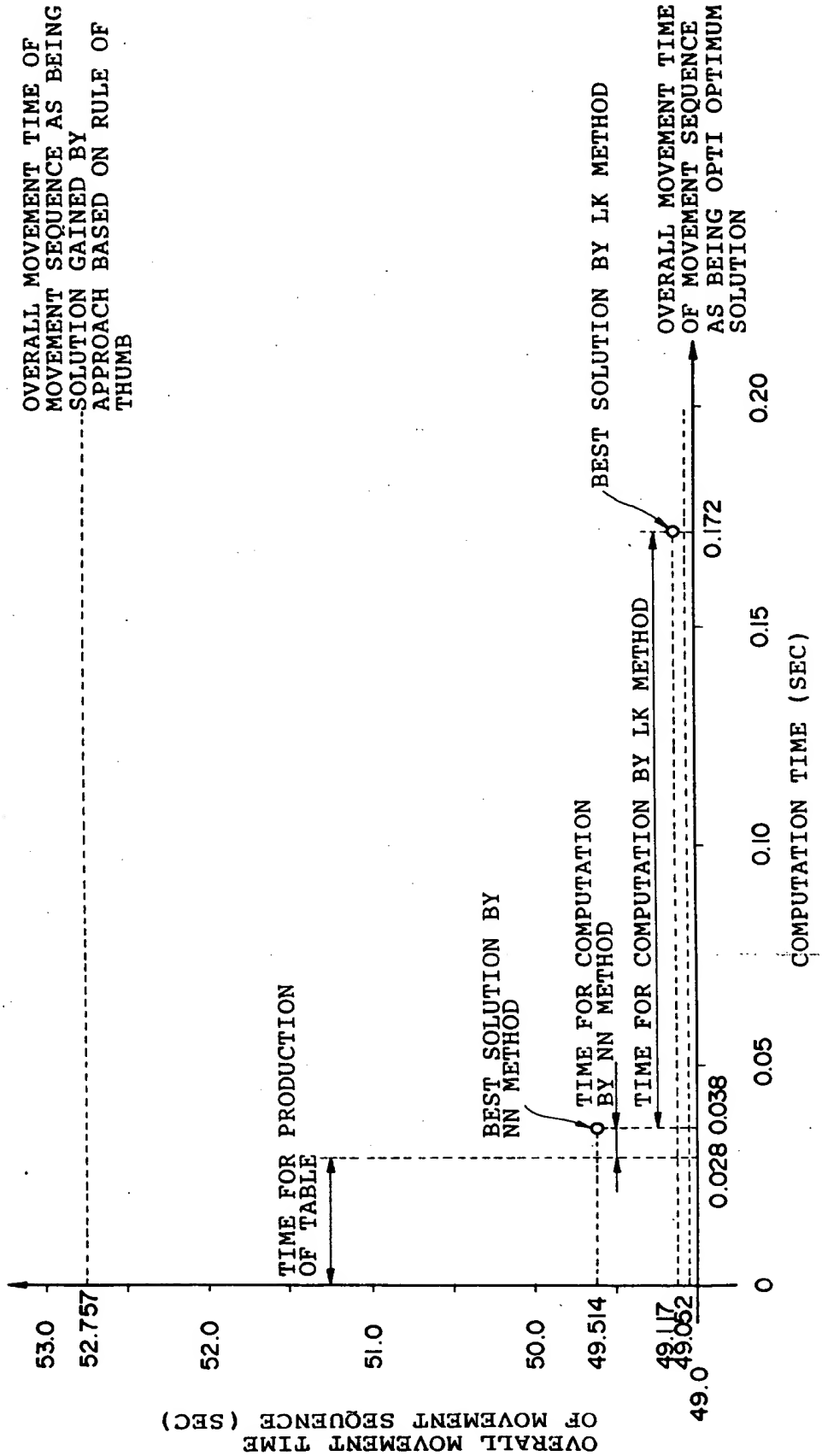


Fig.24

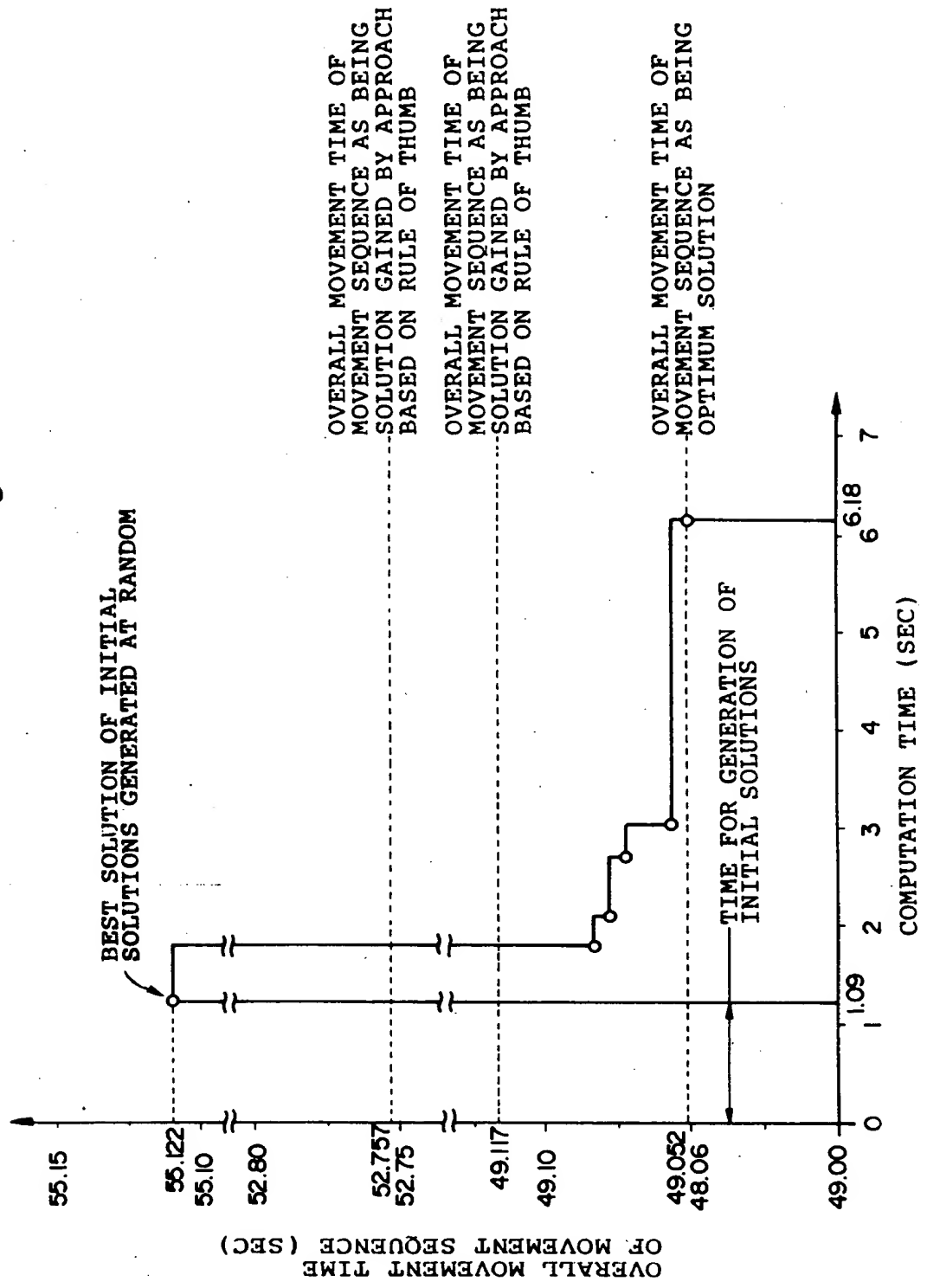
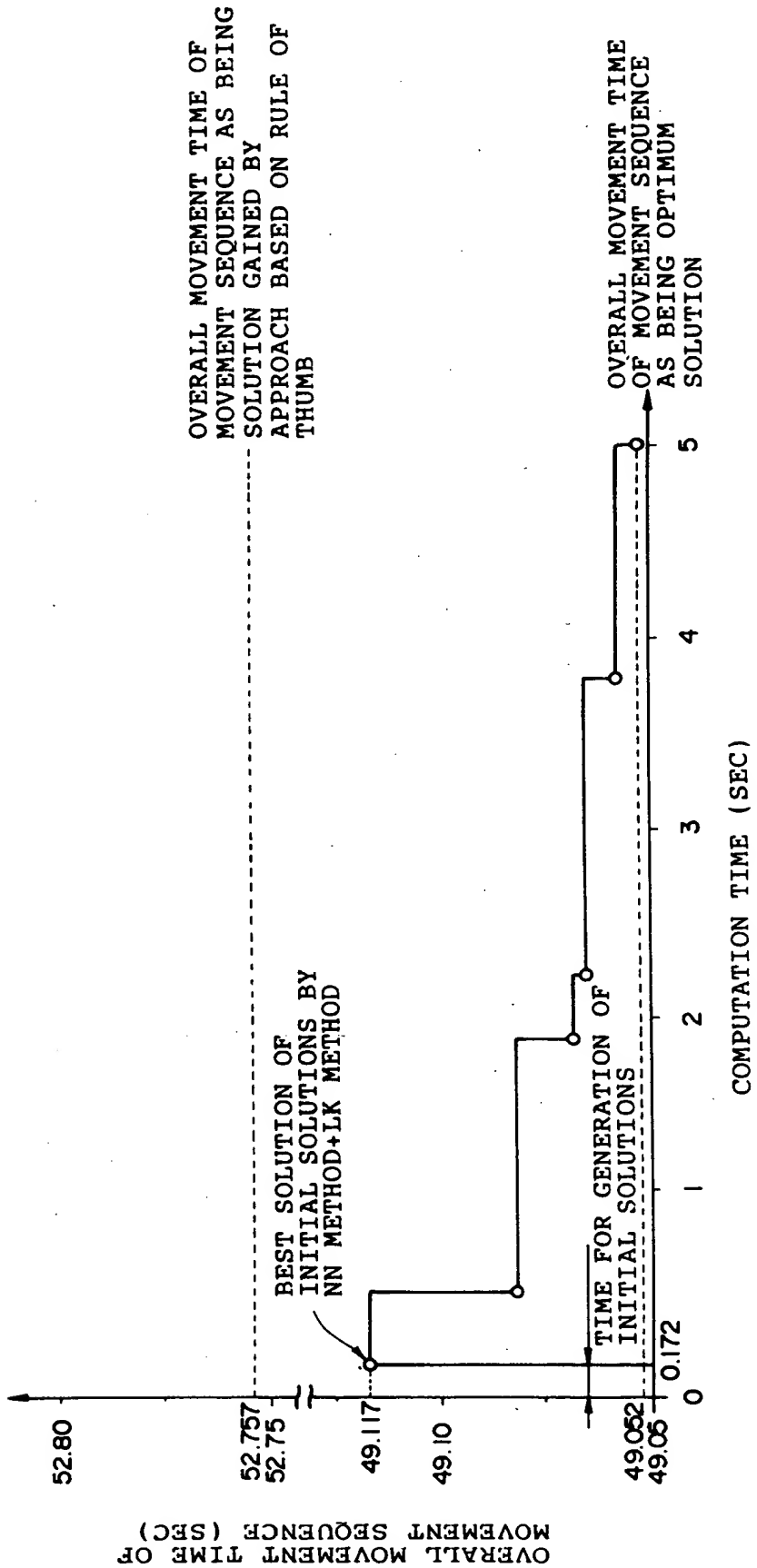

OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE AS BEING SOLUTION GAINED BY APPROACH BASED ON RULE OF THUMB
OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE AS BEING SOLUTION GAINED BY APPROACH BASED ON RULE OF THUMB
OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE AS BEING OPTIMUM SOLUTION
BEST SOLUTION OF INITIAL SOLUTIONS GENERATED AT RANDOM
TIME FOR GENERATION OF INITIAL SOLUTIONS
1.09
6.18
COMPUTATION TIME (SEC)
0
1
2
3
4
5
6
7
55.15
55.122
55.10
52.80
52.757
52.75
49.117
49.10
49.052
48.06
49.00
OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE (SEC)

Fig.25


OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE AS BEING SOLUTION GAINED BY APPROACH BASED ON RULE OF THUMB
BEST SOLUTION OF INITIAL SOLUTIONS BY NN METHOD+LK METHOD
TIME FOR GENERATION OF INITIAL SOLUTIONS
OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE AS BEING OPTIMUM SOLUTION
52.80
52.757
52.75
49.117
49.10
49.052
49.05
0.172
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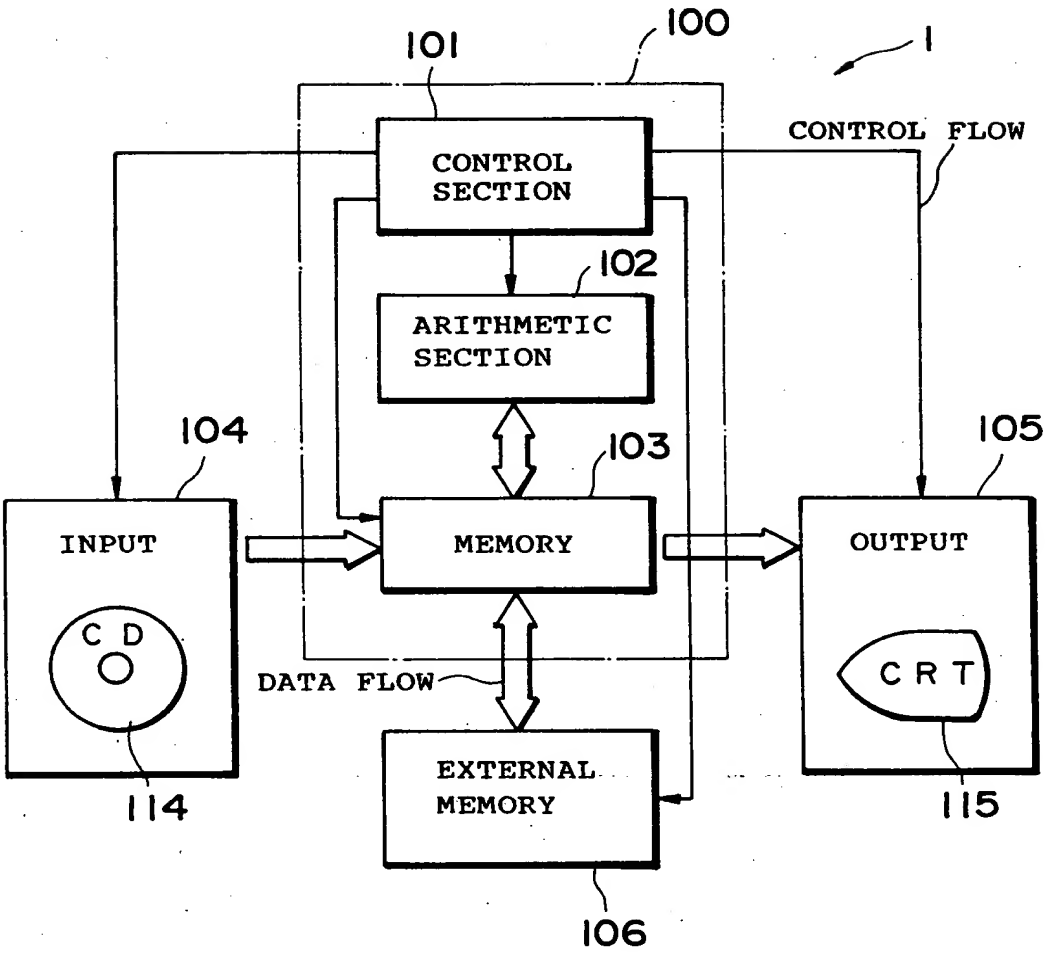
5
COMPUTATION TIME (SEC)
OVERALL MOVEMENT TIME OF MOVEMENT SEQUENCE (SEC)

Fig.26


101
100
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CONTROL FLOW
CONTROL SECTION
102
ARITHMETIC SECTION
104
103
105
INPUT
MEMORY
OUTPUT
C D
DATA FLOW
C R T
EXTERNAL MEMORY
114
115
106

Fig. 27

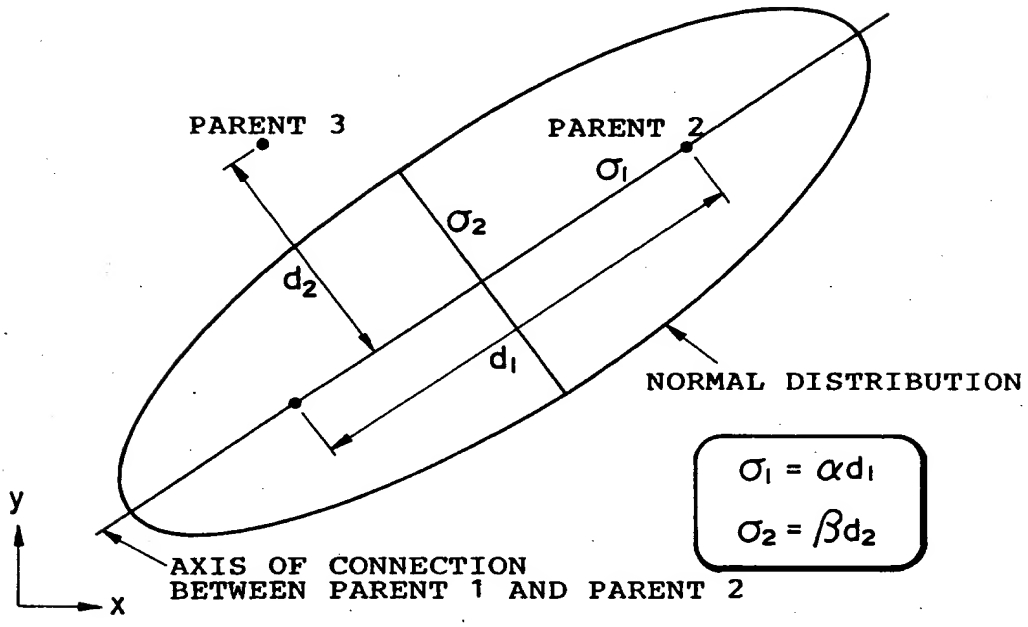

PARENT 3
PARENT 2
σ_1
σ_2
d_2
d_1
NORMAL DISTRIBUTION
$\sigma_1 = \alpha d_1$
$\sigma_2 = \beta d_2$
y
x
AXIS OF CONNECTION
BETWEEN PARENT 1 AND PARENT 2

Fig. 28

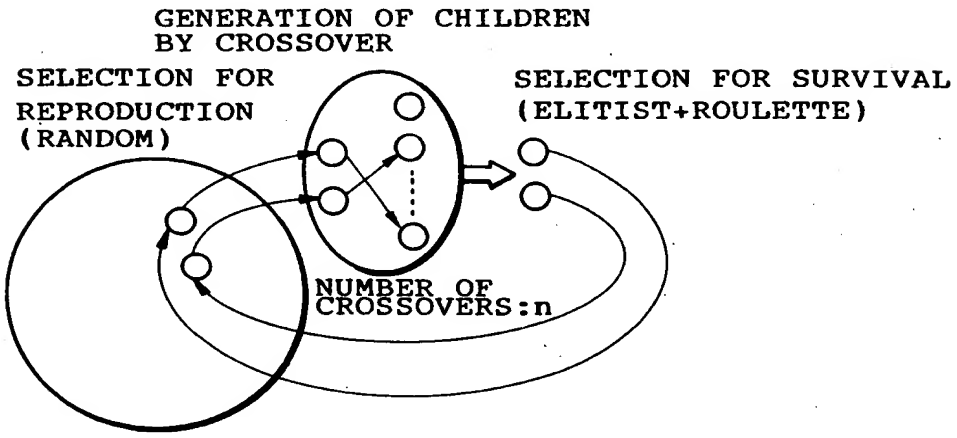

GENERATION OF CHILDREN
BY CROSSOVER
SELECTION FOR
REPRODUCTION
(RANDOM)
SELECTION FOR SURVIVAL
(ELITIST+ROULETTE)
NUMBER OF
CROSSOVERS:n

Fig.29

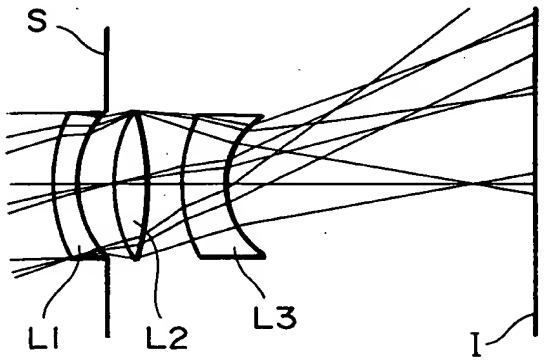
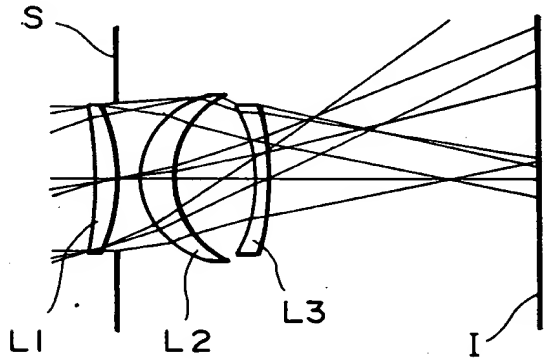


Fig.30



FOCAL STANDARD

Fig. 31

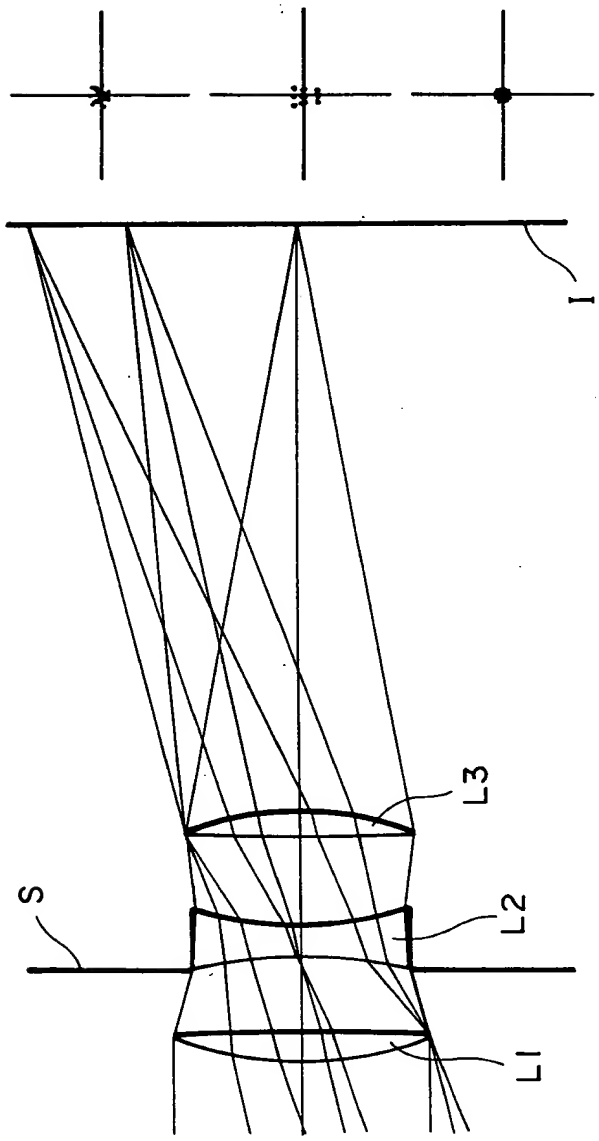


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Fig.32

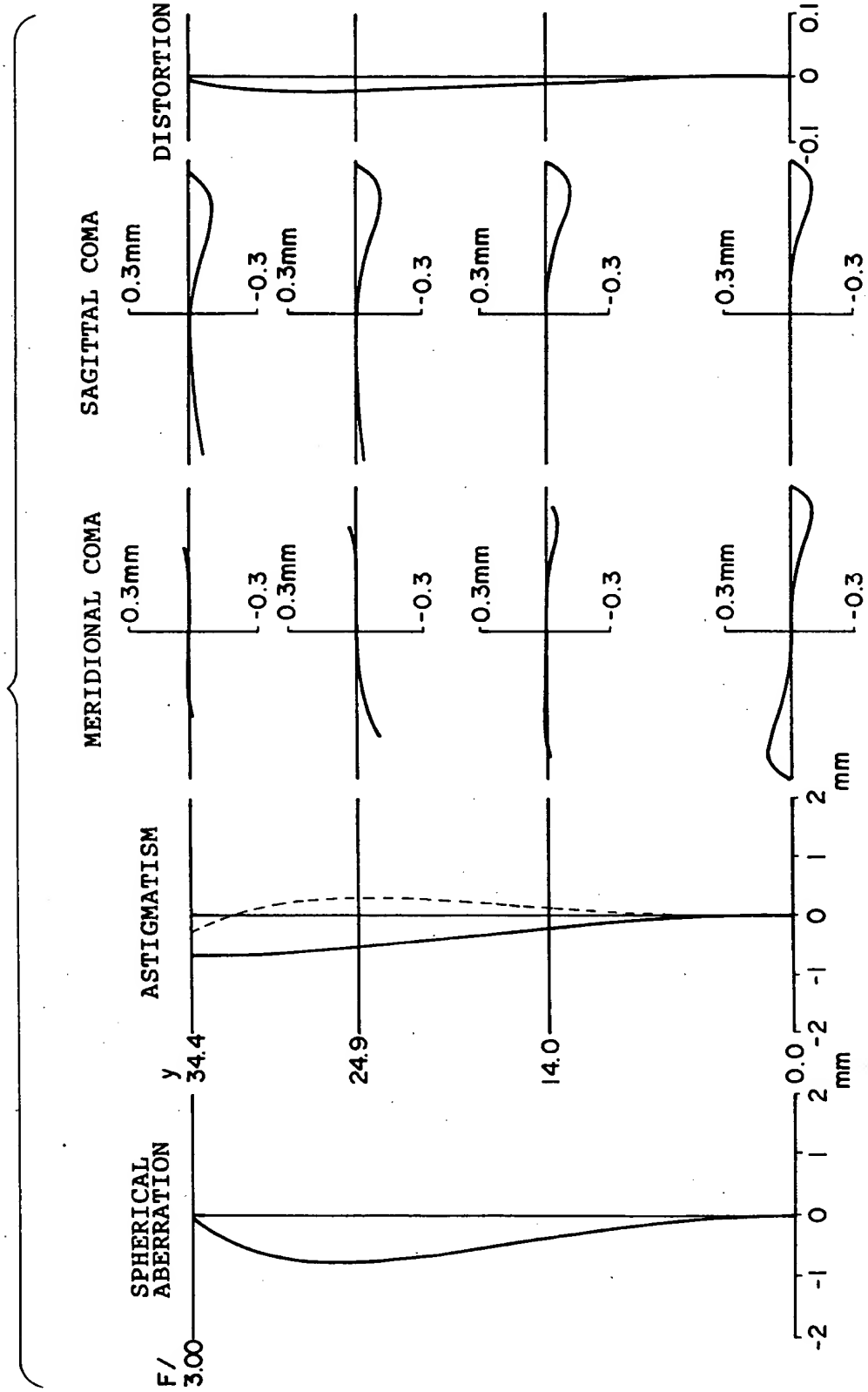


Fig. 33

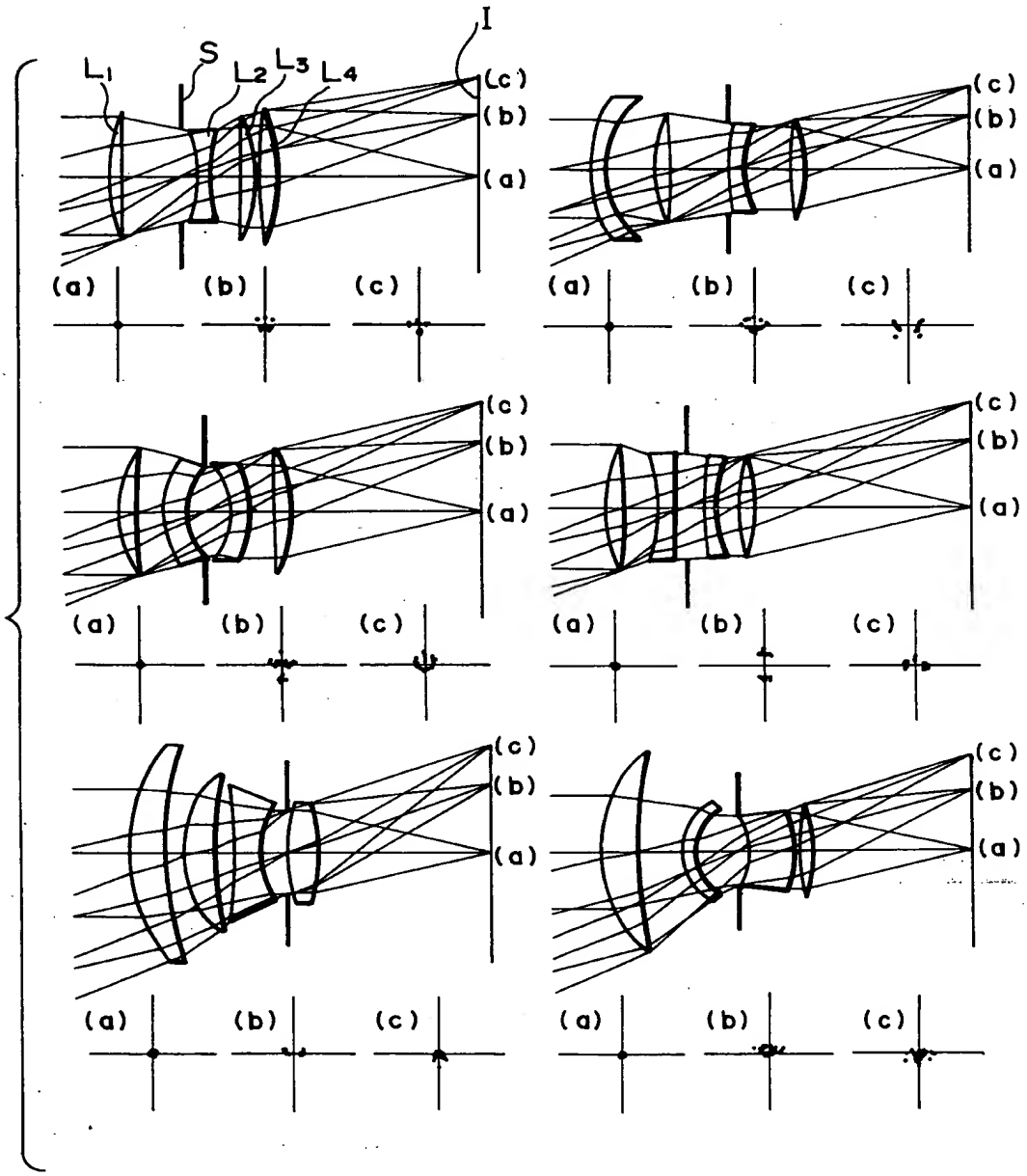


Fig.34

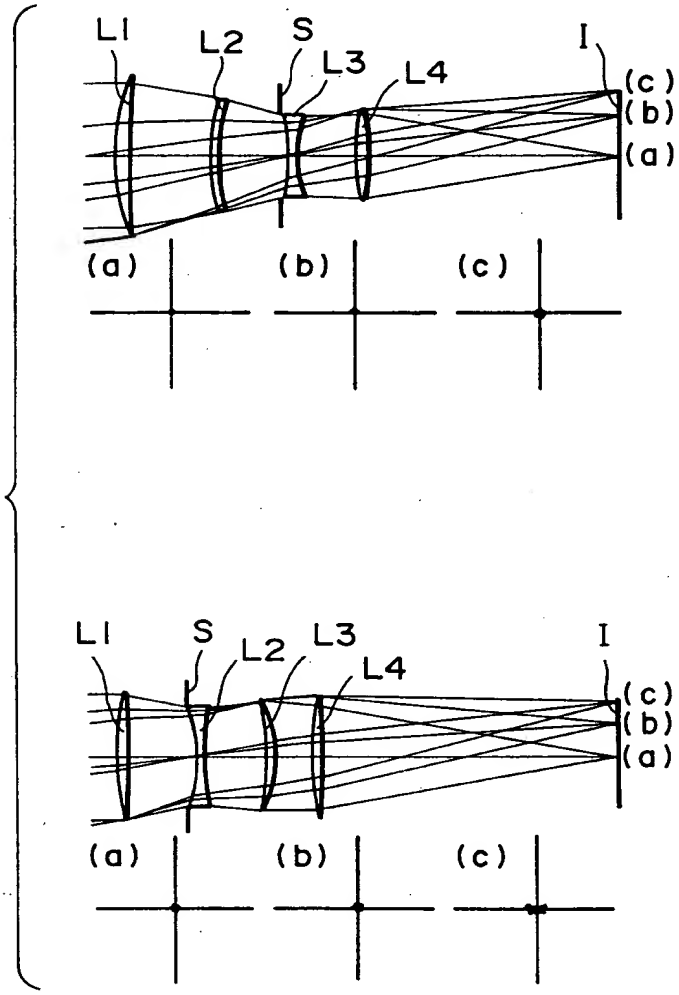


Fig. 35

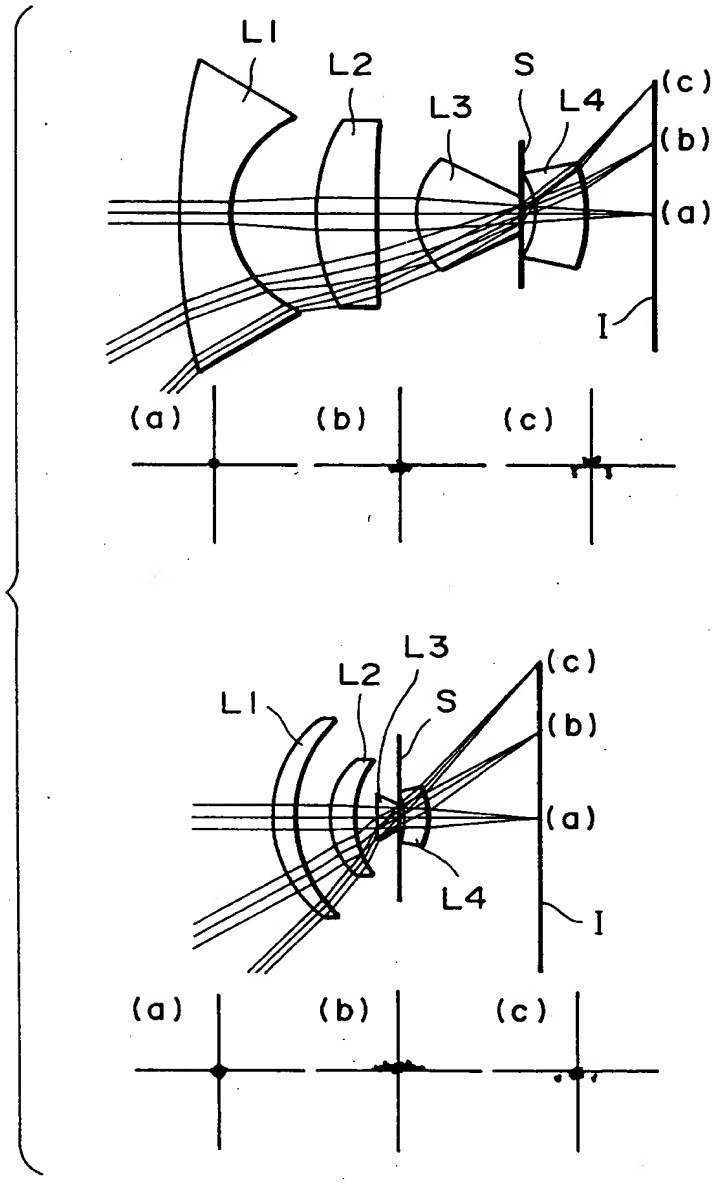
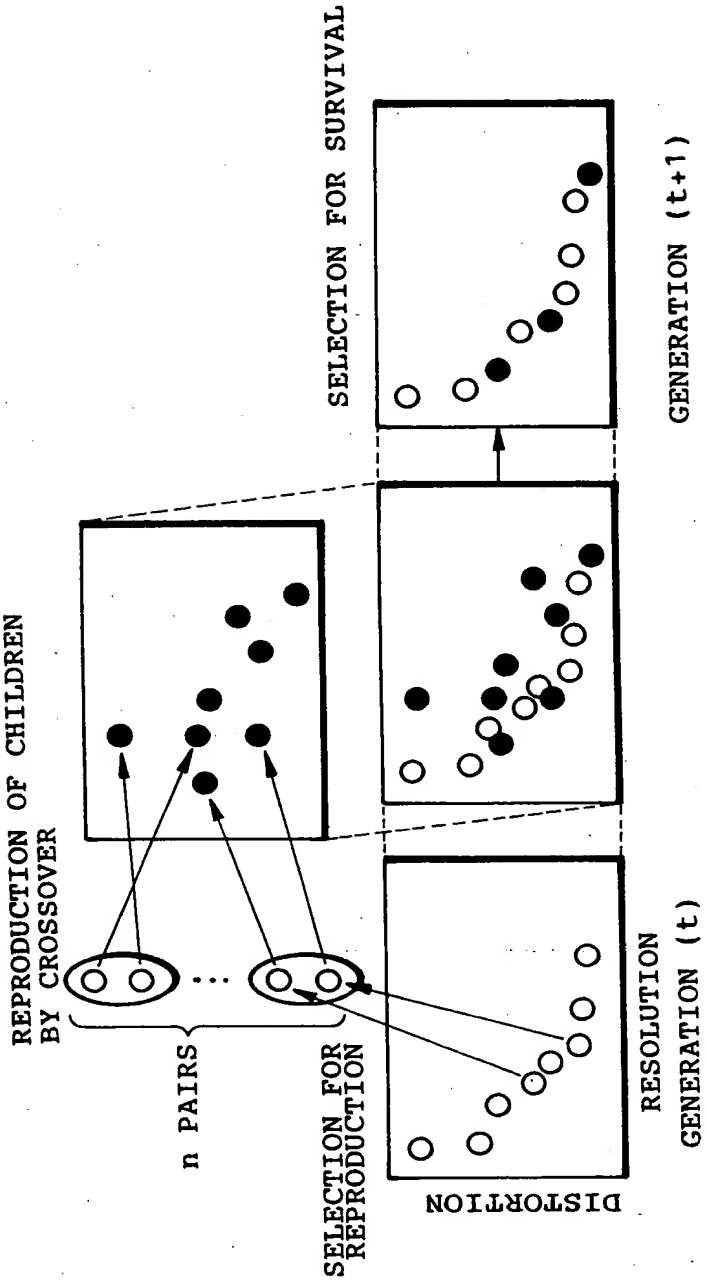
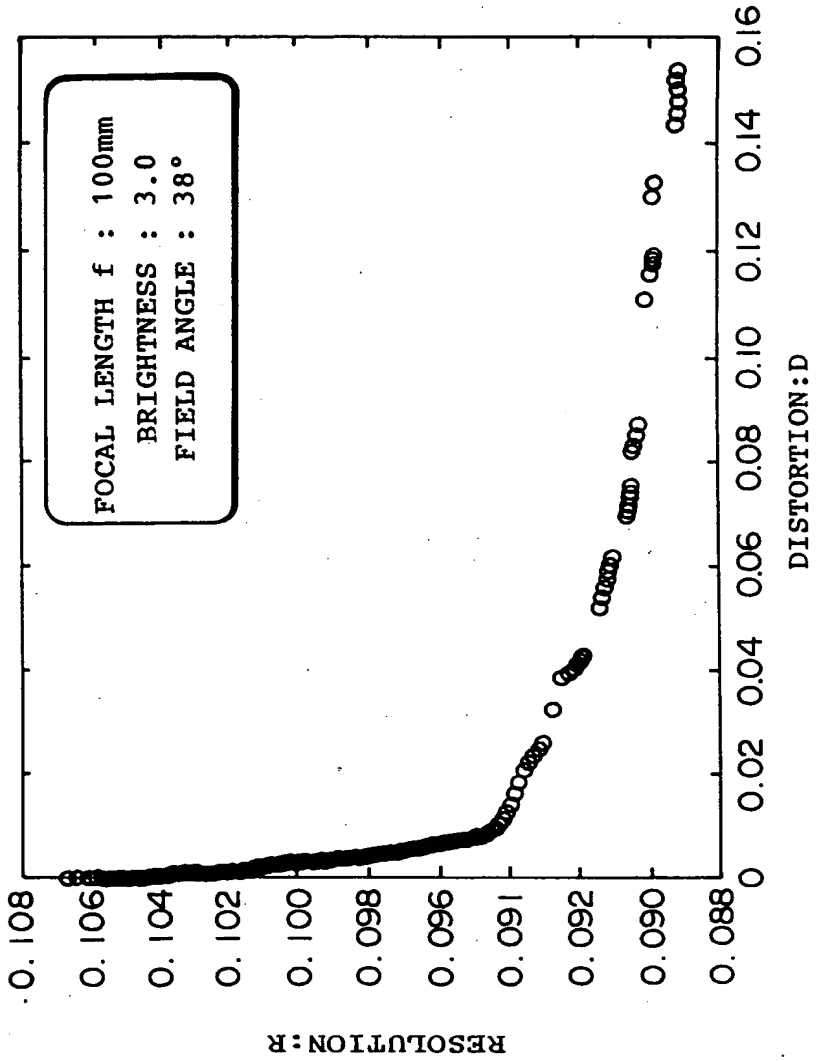


Fig. 36


SELECTION FOR SURVIVAL
GENERATION (t+1)
REPRODUCTION OF CHILDREN BY CROSSOVER
n PAIRS
SELECTION FOR REPRODUCTION
DISTORTION
RESOLUTION
GENERATION (t)

EXPRESS MAIL NO. EV 339 150 245 US

Fig.37



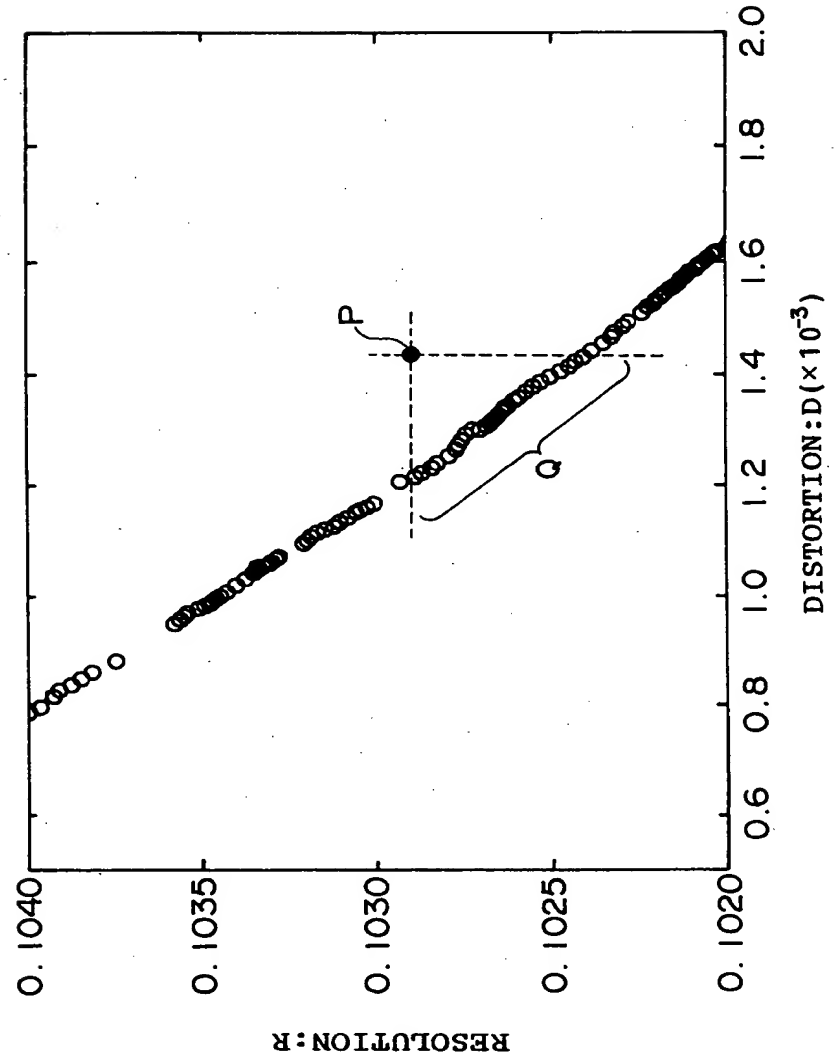

P
Q
0.1040
0.1035
0.1030
0.1025
0.1020
RESOLUTION:R
0.6
0.8
1.0
1.2
1.4
1.6
1.8
2.0
DISTORTION:D(×10⁻³)

Fig. 38

Fig. 39

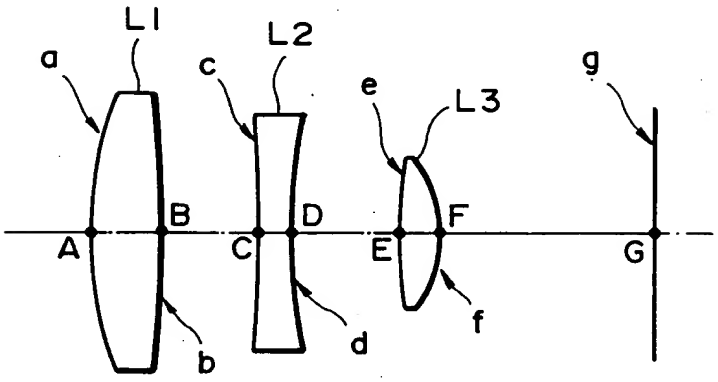


Fig. 41

GENE REPRESENTATION:

a	b	c	d	e	d1	d2	d3	d4	d5

TOKKYO "SYSTEM"

Fig. 40

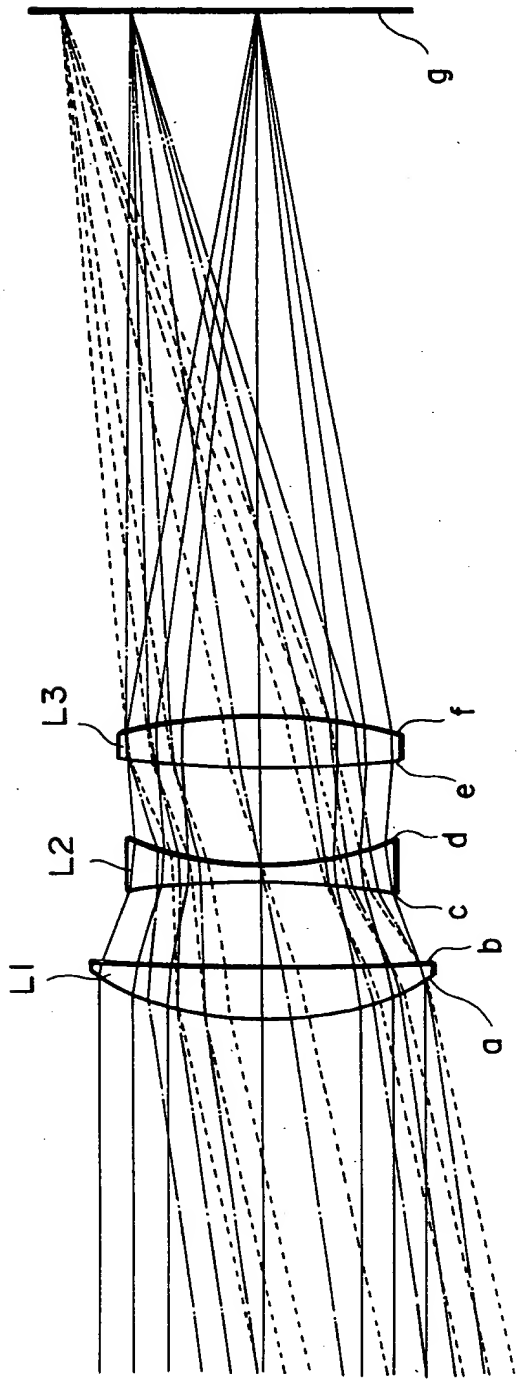


Fig. 42

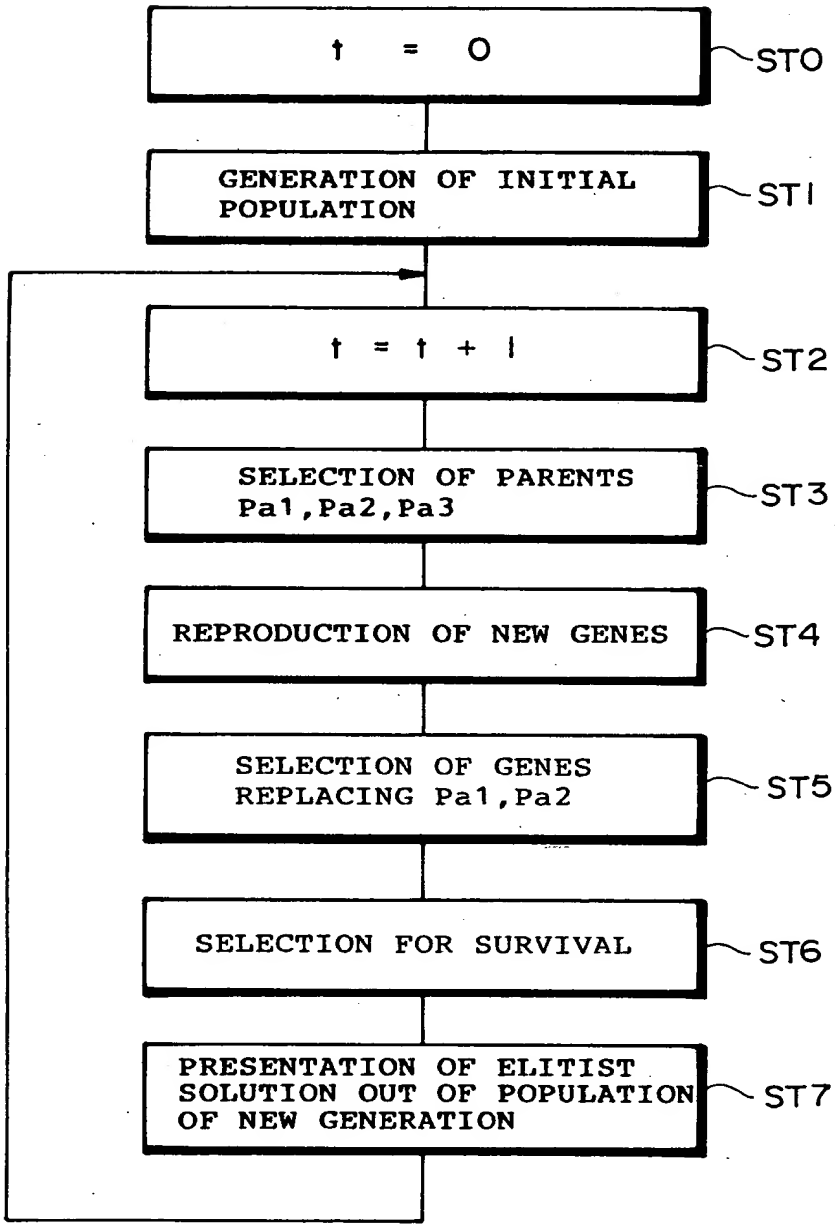

t = 0
ST0
GENERATION OF INITIAL POPULATION
ST1
t = t + 1
ST2
SELECTION OF PARENTS Pa1,Pa2,Pa3
ST3
REPRODUCTION OF NEW GENES
ST4
SELECTION OF GENES REPLACING Pa1,Pa2
ST5
SELECTION FOR SURVIVAL
ST6
PRESENTATION OF ELITIST SOLUTION OUT OF POPULATION OF NEW GENERATION
ST7

Fig. 43

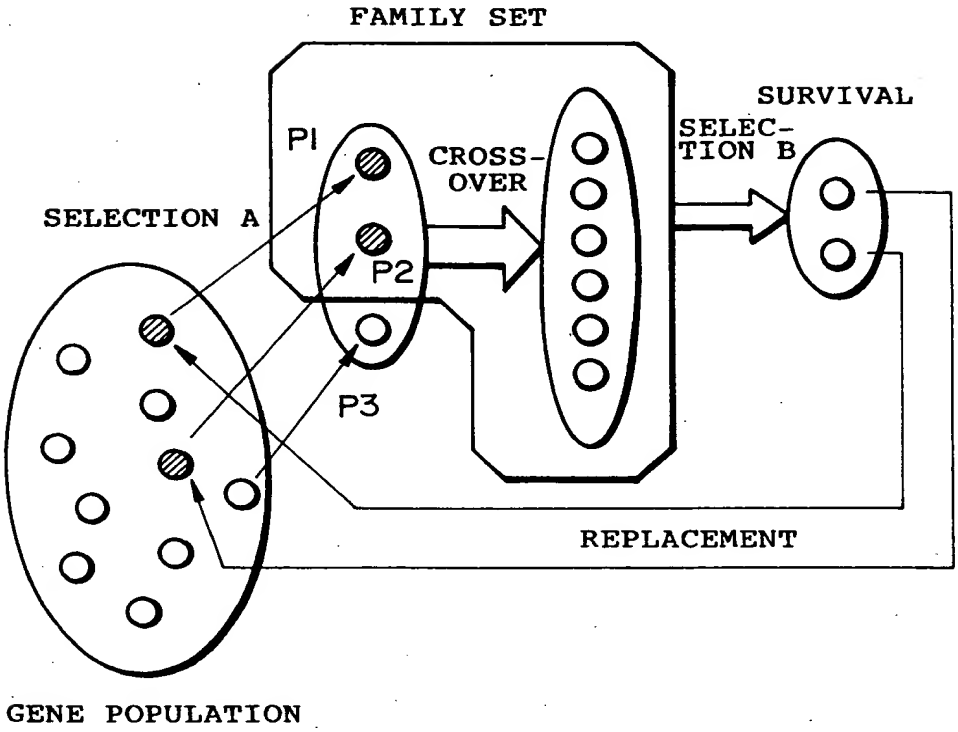

FAMILY SET
SURVIVAL SELEC-TION B
P1
CROSS-OVER
SELECTION A
P2
P3
REPLACEMENT
GENE POPULATION

Fig. 44

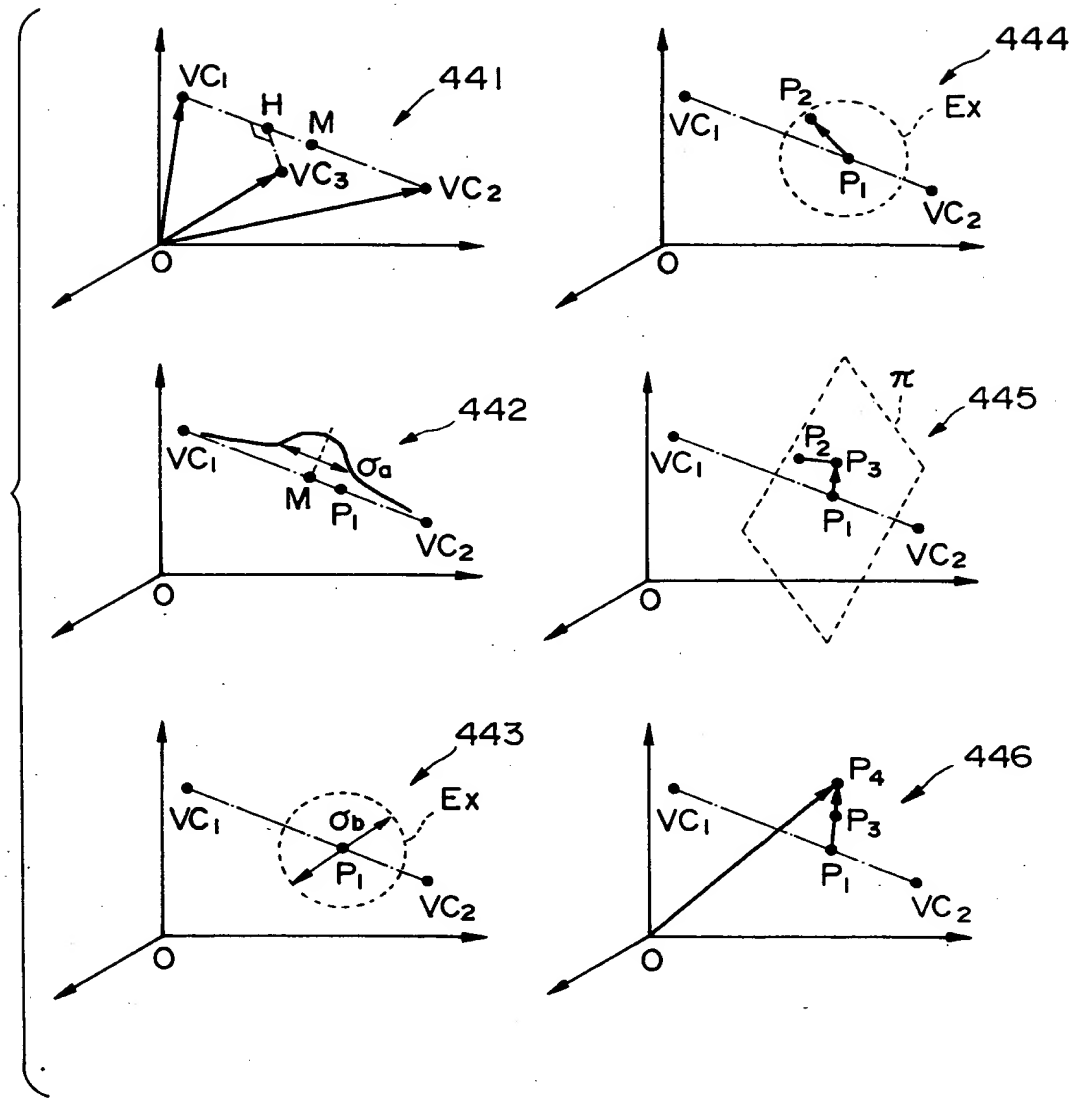
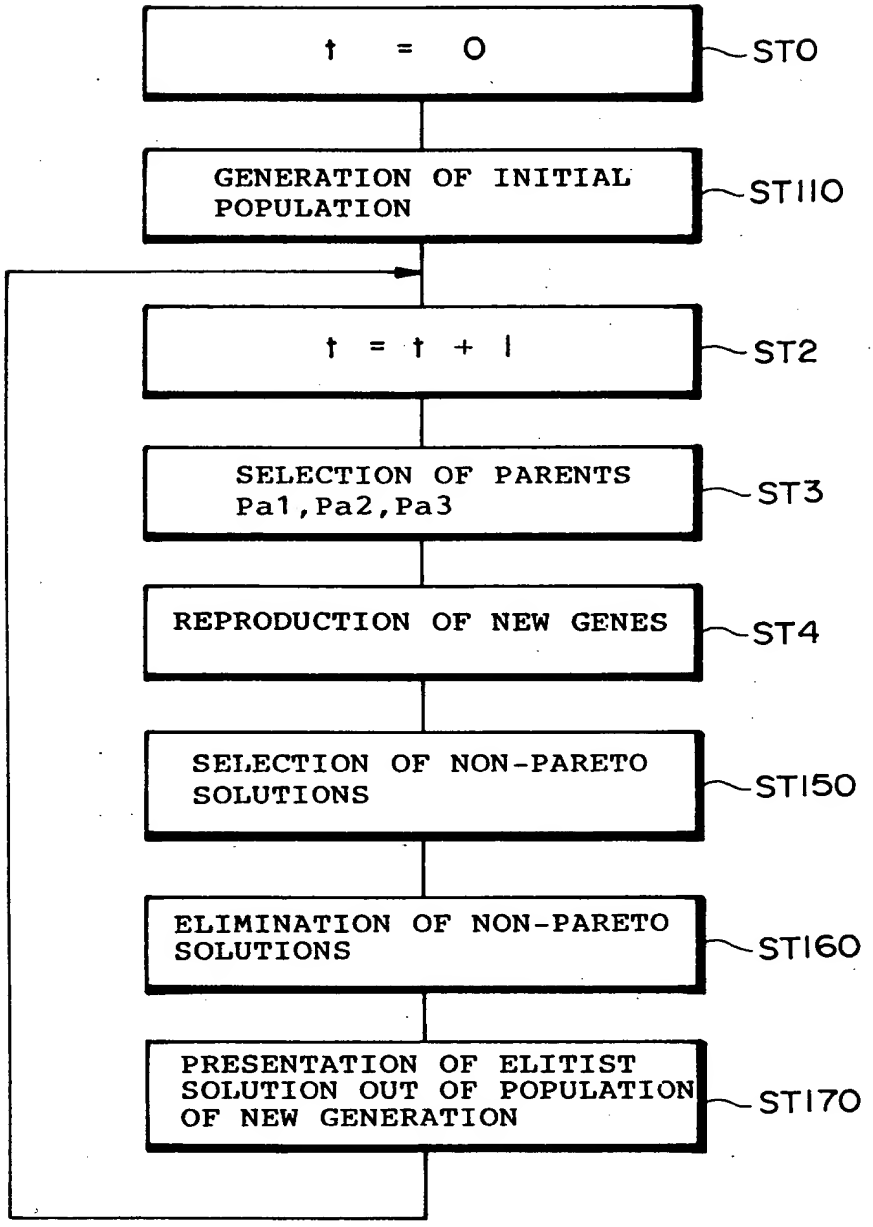

441
VC1
H
M
VC3
VC2
O
444
P2
Ex
VC1
P1
VC2
O
442
VC1
σa
M
P1
VC2
O
445
π
P2
P3
VC1
P1
VC2
O
443
VC1
σb
Ex
P1
VC2
O
446
P4
P3
VC1
P1
VC2
O

Fig. 45


t = 0
ST0
GENERATION OF INITIAL POPULATION
ST110
t = t + 1
ST2
SELECTION OF PARENTS Pa1, Pa2, Pa3
ST3
REPRODUCTION OF NEW GENES
ST4
SELECTION OF NON-PARETO SOLUTIONS
ST150
ELIMINATION OF NON-PARETO SOLUTIONS
ST160
PRESENTATION OF ELITIST SOLUTION OUT OF POPULATION OF NEW GENERATION
ST170

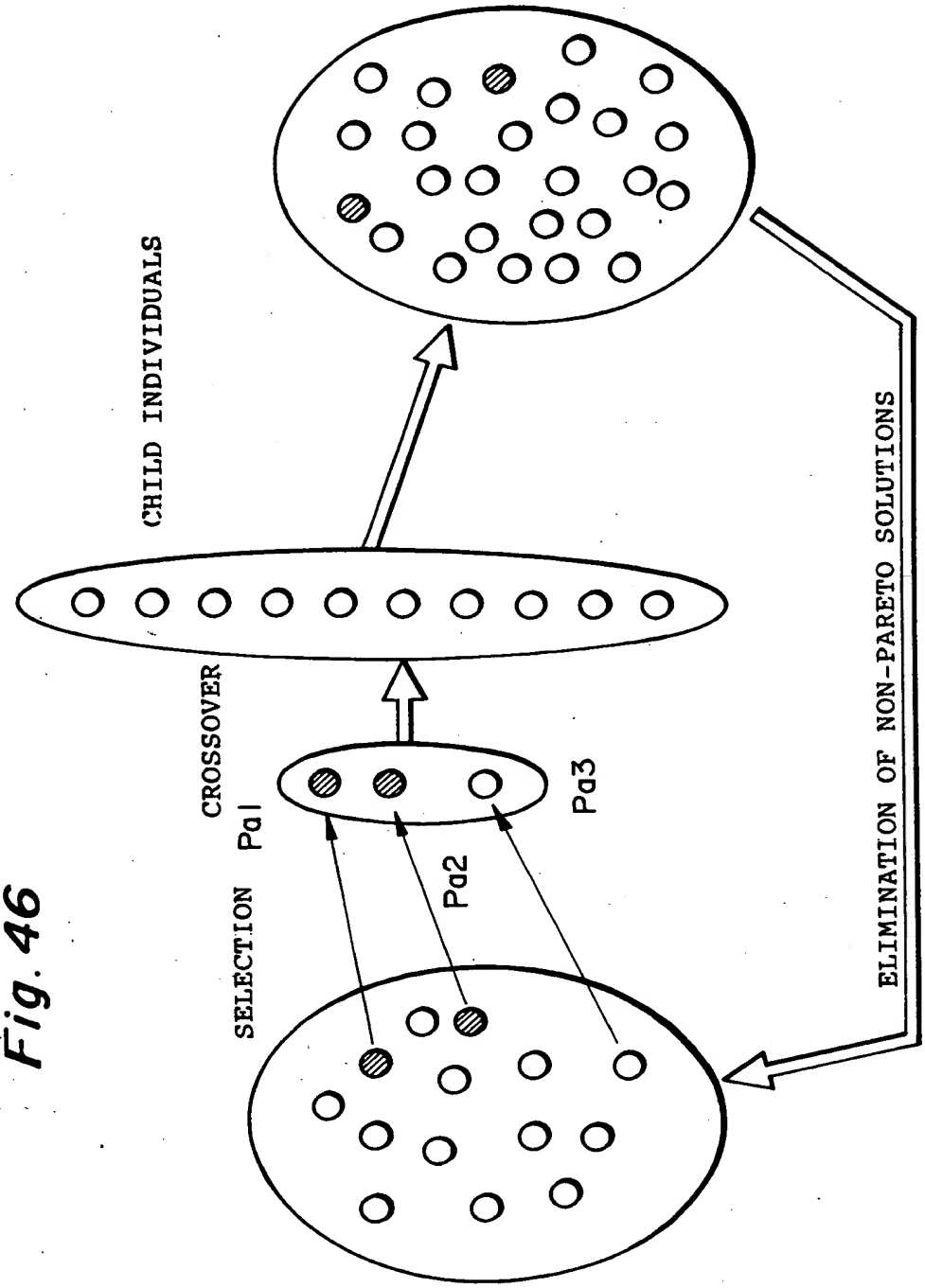

CHILD INDIVIDUALS
CROSSOVER
Pa1
Pa2
Pa3
SELECTION
ELIMINATION OF NON-PARETO SOLUTIONS

Fig. 46

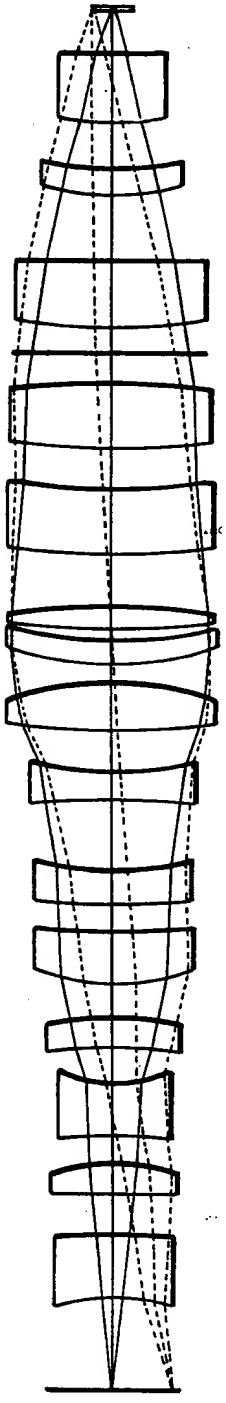
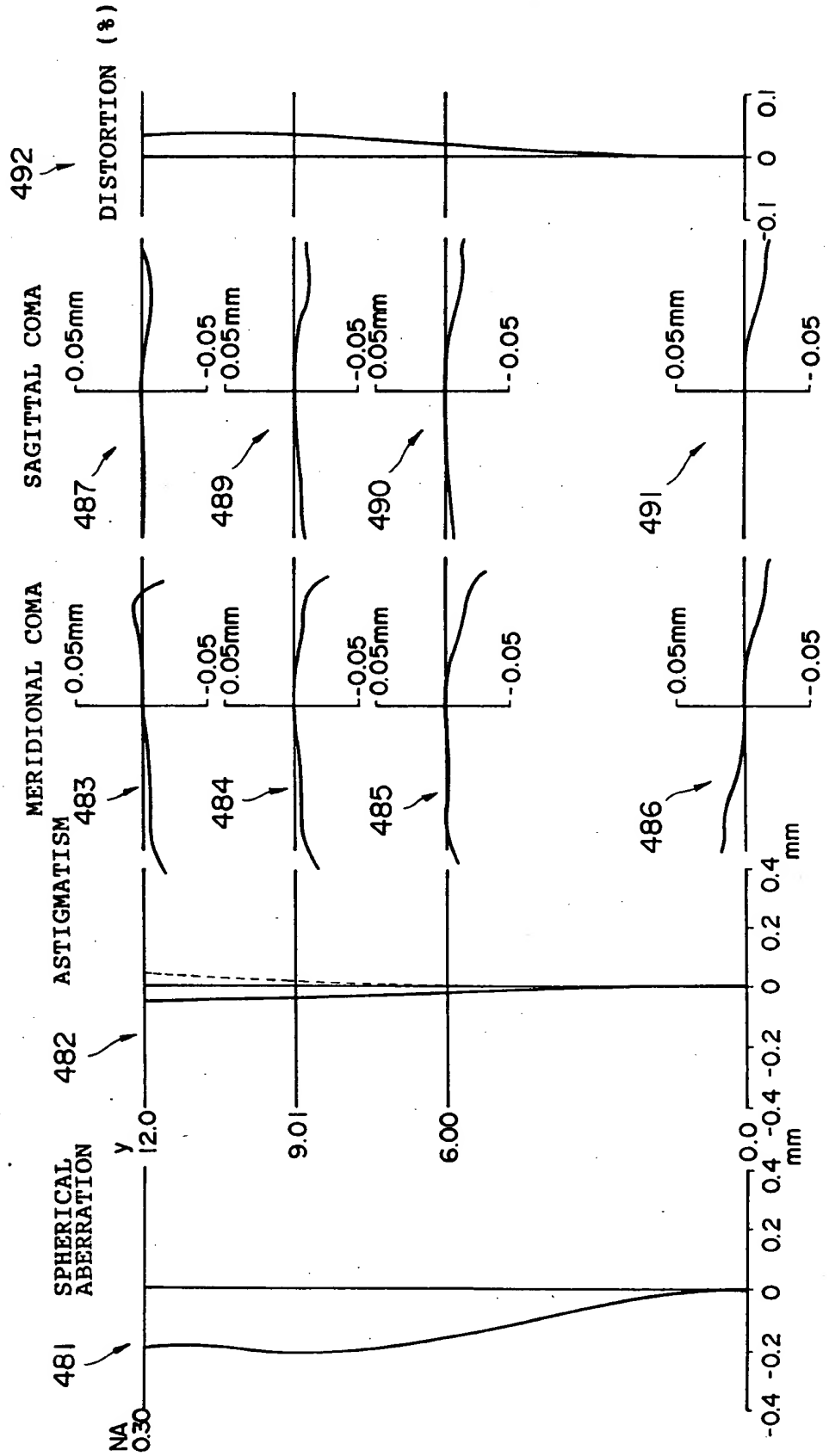


Fig. 47

EPO - DG 1

Fig. 48



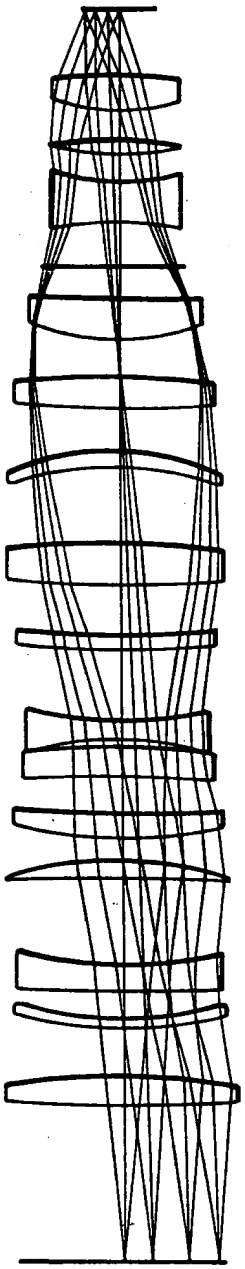


Fig. 49